



SEQUENCE LISTING

Lehmann, Martin
Lassen, Soren F

<120> Improved Phytases

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<160> 98

<170> PatentIn version 3.2

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35 40 45

Phe Val Gln Val Leu Ala Arg His Gly Ala Arg Ser Pro Thr His Ser
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Lys Thr Lys Ala Tyr Ala Ala Thr Ile Ala Ala Ile Gln Lys Ser Ala
65 70 75 80

Thr Ala Phe Pro Gly Lys Tyr Ala Phe Leu Gln Ser Tyr Asn Tyr Ser
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Leu Asp Ser Glu Glu Leu Thr Pro Phe Gly Arg Asn Gln Leu Arg Asp
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Leu Gly Ala Gln Phe Tyr Glu Arg Tyr Asn Ala Leu Thr Arg His Ile
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Asn Pro Phe Val Arg Ala Thr Asp Ala Ser Arg Val His Glu Ser Ala
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Glu Lys Phe Val Glu Gly Phe Gln Thr Ala Arg Gln Asp Asp His His

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TECH CENTER 1600/2900

145 150 155 160
Ala Asn Pro His Gln Pro Ser Pro Arg Val Asp Val Ala Ile Pro Glu
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Gly Ser Ala Tyr Asn Asn Thr Leu Glu His Ser Leu Cys Thr Ala Phe
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Glu Ser Ser Thr Val Gly Asp Asp Ala Val Ala Asn Phe Thr Ala Val
195 200 205

Phe Ala Pro Ala Ile Ala Gln Arg Leu Glu Ala Asp Leu Pro Gly Val
210 215 220

Gln Leu Ser Thr Asp Asp Val Val Asn Leu Met Ala Met Cys Pro Phe
225 230 235 240

Glu Thr Val Ser Leu Thr Asp Asp Ala His Thr Leu Ser Pro Phe Cys
245 250 255

Asp Leu Phe Thr Ala Thr Glu Trp Thr Gln Tyr Asn Tyr Leu Leu Ser
260 265 270

Leu Asp Lys Tyr Tyr Gly Gly Gly Asn Pro Leu Gly Pro Val
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Gln Gly Val Gly Trp Ala Asn Glu Leu Met Ala Arg Leu Thr Arg Ala
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Pro Val His Asp His Thr Cys Val Asn Asn Thr Leu Asp Ala Ser Pro
305 310 315 320

Ala Thr Phe Pro Leu Asn Ala Thr Leu Tyr Ala Asp Phe Ser His Asp
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Ser Asn Leu Val Ser Ile Phe Trp Ala Leu Gly Leu Tyr Asn Gly Thr
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Ala Pro Leu Ser Gln Thr Ser Val Glu Ser Val Ser Gln Thr Asp Gly
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Tyr Ala Ala Ala Trp Thr Val Pro Phe Ala Ala Arg Ala Tyr Val Glu
370 375 380

Met Met Gln Cys Arg Ala Glu Lys Glu Pro Leu Val Arg Val Leu Val
385 390 395 400

Asn Asp Arg Val Met Pro Leu His Gly Cys Pro Thr Asp Lys Leu Gly
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35 40 45

Phe Val Gln Val Leu Ala Arg His Gly Ala Arg Ser Pro Thr Asp Ser
50 55 60

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Thr Ala Leu Pro Gly Lys Tyr Ala Phe Leu Lys Ser Tyr Asn Tyr Ser
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Met Gly Ser Glu Asn Leu Thr Pro Phe Gly Arg Asn Gln Leu Gln Asp
100 105 110

Leu Gly Ala Gln Phe Tyr Arg Arg Tyr Asp Thr Leu Thr Arg His Ile
115 120 125

Asn Pro Phe Val Arg Ala Ala Asp Ser Ser Arg Val His Glu Ser Ala
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Glu Lys Phe Val Glu Gly Phe Gln Asn Ala Arg Gln Gly Asp Pro His
145 150 155 160

Ala Asn Pro His Gln Pro Ser Pro Arg Val Asp Val Val Ile Pro Glu
165 170 175

Gly Thr Ala Tyr Asn Asn Thr Leu Glu His Ser Ile Cys Thr Ala Phe
180 185 190

Glu Ala Ser Thr Val Gly Asp Ala Ala Ala Asp Asn Phe Thr Ala Val
195 200 205

Phe Ala Pro Ala Ile Ala Lys Arg Leu Glu Ala Asp Leu Pro Gly Val
210 215 220

Gln Leu Ser Ala Asp Asp Val Val Asn Leu Met Ala Met Cys Pro Phe
225 230 235 240

Glu Thr Val Ser Leu Thr Asp Asp Ala His Thr Leu Ser Pro Phe Cys
245 250 255

Asp Leu Phe Thr Ala Ala Glu Trp Thr Gln Tyr Asn Tyr Leu Leu Ser
260 265 270

Leu Asp Lys Tyr Tyr Gly Gly Gly Asn Pro Leu Gly Pro Val
275 280 285

Gln Gly Val Gly Trp Ala Asn Glu Leu Ile Ala Arg Leu Thr Arg Ser
290 295 300

Pro Val His Asp His Thr Cys Val Asn Asn Thr Leu Asp Ala Asn Pro
305 310 315 320

Ala Thr Phe Pro Leu Asn Ala Thr Leu Tyr Ala Asp Phe Ser His Asp
325 330 335

Ser Asn Leu Val Ser Ile Phe Trp Ala Leu Gly Leu Tyr Asn Gly Thr
340 345 350

Lys Pro Leu Ser Gln Thr Thr Val Glu Asp Ile Thr Arg Thr Asp Gly

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Tyr Ala Ala Ala Trp Thr Val Pro Phe Ala Ala Arg Ala Tyr Ile Glu
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Met Met Gln Cys Arg Ala Glu Lys Gln Pro Leu Val Arg Val Leu Val
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Asn Asp Arg Val Met Pro Leu His Gly Cys Ala Val Asp Asn Leu Gly
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35 40 45

Phe Ala Gln Val Leu Ser Arg His Gly Ala Arg Tyr Pro Thr Glu Ser
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65 70 75 80

Thr Thr Phe Asp Gly Lys Tyr Ala Phe Leu Lys Thr Tyr Asn Tyr Ser
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Leu Gly Ala Asp Asp Leu Thr Pro Phe Gly Glu Gln Glu Leu Val Asn
100 105 110

Ser Gly Ile Lys Phe Tyr Gln Arg Tyr Glu Ser Leu Thr Arg Asn Ile
115 120 125

Ile Pro Phe Ile Arg Ser Ser Gly Ser Ser Arg Val Ile Ala Ser Gly
130 135 140

Glu Lys Phe Ile Glu Gly Phe Gln Ser Thr Lys Leu Lys Asp Pro Arg
145 150 155 160

Ala Gln Pro Gly Gln Ser Ser Pro Lys Ile Asp Val Val Ile Ser Glu
165 170 175

Ala Ser Ser Ser Asn Asn Thr Leu Asp Pro Gly Thr Cys Thr Val Phe
180 185 190

Glu Asp Ser Glu Leu Ala Asp Thr Val Glu Ala Asn Phe Thr Ala Thr
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Phe Ala Pro Ser Ile Arg Gln Arg Leu Glu Asn Asp Leu Ser Gly Val
210 215 220

Thr Leu Thr Asp Thr Glu Val Thr Tyr Leu Met Asp Met Cys Ser Phe
225 230 235 240

Asp Thr Ile Ser Thr Ser Thr Val Asp Thr Lys Leu Ser Pro Phe Cys
245 250 255

Asp Leu Phe Thr His Asp Glu Trp Ile His Tyr Asp Tyr Leu Gln Ser
260 265 270

Leu Lys Lys Tyr Tyr Gly His Gly Ala Gly Asn Pro Leu Gly Pro Thr
275 280 285

Gln Gly Val Gly Tyr Ala Asn Glu Leu Ile Ala Arg Leu Thr His Ser
290 295 300

Pro Val His Asp Asp Thr Ser Ser Asn His Thr Leu Asp Ser Asn Pro
305 310 315 320

Ala Thr Phe Pro Leu Asn Ser Thr Leu Tyr Ala Asp Phe Ser His Asp
325 330 335

Asn Gly Ile Ile Ser Ile Leu Phe Ala Leu Gly Leu Tyr Asn Gly Thr
340 345 350

Lys Pro Leu Ser Thr Thr Thr Val Glu Asn Ile Thr Gln Thr Asp Gly
355 360 365

Phe Ser Ser Ala Trp Thr Val Pro Phe Ala Ser Arg Leu Tyr Val Glu
370 375 380

Met Met Gln Cys Gln Ala Glu Gln Glu Pro Leu Val Arg Val Leu Val
385 390 395 400

Asn Asp Arg Val Val Pro Leu His Gly Cys Pro Ile Asp Ala Leu Gly
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35 40 45

Phe Ala Gln Val Leu Ser Arg His Gly Ala Arg Tyr Pro Thr Glu Ser
50 55 60

Lys Gly Lys Lys Tyr Ser Ala Leu Ile Glu Glu Ile Gln Gln Asn Val
65 70 75 80

Thr Thr Phe Asp Gly Lys Tyr Ala Phe Leu Lys Thr Tyr Asn Tyr Ser
85 90 95

Leu Gly Ala Asp Asp Leu Thr Pro Phe Gly Glu Gln Glu Leu Val Asn
100 105 110

Ser Gly Ile Lys Phe Tyr Gln Arg Tyr Glu Ser Leu Thr Arg Asn Ile
115 120 125

Ile Pro Phe Ile Arg Ser Ser Gly Ser Ser Arg Val Ile Ala Ser Gly
130 135 140

Glu Lys Phe Ile Glu Gly Phe Gln Ser Thr Lys Leu Lys Asp Pro Arg
145 150 155 160

Ala Gln Pro Gly Gln Ser Ser Pro Lys Ile Asp Val Val Ile Ser Glu
165 170 175

Ala Ser Ser Ser Asn Asn Thr Leu Asp Pro Gly Thr Cys Thr Val Phe
180 185 190

Glu Asp Ser Glu Leu Ala Asp Thr Val Glu Ala Asn Phe Thr Ala Thr
195 200 205

Phe Ala Pro Ser Ile Arg Gln Arg Leu Glu Asn Asp Leu Ser Gly Val
210 215 220

Thr Leu Thr Asp Thr Glu Val Thr Tyr Leu Met Asp Met Cys Ser Phe
225 230 235 240

Asp Thr Ile Ser Thr Ser Thr Val Asp Thr Lys Leu Ser Pro Phe Cys
245 250 255

Asp Leu Phe Thr His Asp Glu Trp Ile His Tyr Asp Tyr Leu Arg Ser
260 265 270

Leu Lys Lys Tyr Tyr Gly His Gly Ala Gly Asn Pro Leu Gly Pro Thr
275 280 285

Gln Gly Val Gly Tyr Ala Asn Glu Leu Ile Ala Arg Leu Thr His Ser
290 295 300

Pro Val His Asp Asp Thr Ser Ser Asn His Thr Leu Asp Ser Asn Pro
305 310 315 320

Ala Thr Phe Pro Leu Asn Ser Thr Leu Tyr Ala Asp Phe Ser His Asp
325 330 335

Asn Gly Ile Ile Ser Ile Leu Phe Ala Leu Gly Leu Tyr Asn Gly Thr
340 345 350

Lys Pro Leu Ser Thr Thr Val Glu Asn Ile Thr Gln Thr Asp Gly
355 360 365

Phe Ser Ser Ala Trp Thr Val Pro Phe Ala Ser Arg Leu Tyr Val Glu
370 375 380

Met Met Gln Cys Gln Ala Glu Gln Glu Pro Leu Val Arg Val Leu Val
385 390 395 400

Asn Asp Arg Val Val Pro Leu His Gly Cys Pro Ile Asp Ala Leu Gly
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Phe Ala Gln Val Leu Ser Arg His Gly Ala Arg Tyr Pro Thr Asp Ser
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70

75

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Thr Thr Phe Asp Gly Lys Tyr Ala Phe Leu Lys Thr Tyr Asn Tyr Ser
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Leu Gly Ala Asp Asp Leu Thr Pro Phe Gly Glu Gln Glu Leu Val Asn
100 105 110

Ser Gly Ile Lys Phe Tyr Gln Arg Tyr Glu Ser Leu Thr Arg Asn Ile
115 120 125

Val Pro Phe Ile Arg Ser Ser Gly Ser Ser Arg Val Ile Ala Ser Gly
130 135 140

Lys Lys Phe Ile Glu Gly Phe Gln Ser Thr Lys Leu Lys Asp Pro Arg
145 150 155 160

Ala Gln Pro Gly Gln Ser Ser Pro Lys Ile Asp Val Val Ile Ser Glu
165 170 175

Ala Ser Ser Ser Asn Asn Thr Leu Asp Pro Gly Thr Cys Thr Val Phe
180 185 190

Glu Asp Ser Glu Leu Ala Asp Thr Val Glu Ala Asn Phe Thr Ala Thr
195 200 205

Phe Val Pro Ser Ile Arg Gln Arg Leu Glu Asn Asp Leu Ser Gly Val
210 215 220

Thr Leu Thr Asp Thr Glu Val Thr Tyr Leu Met Asp Met Cys Ser Phe
225 230 240

Asp Thr Ile Ser Thr Ser Thr Val Asp Thr Lys Leu Ser Pro Phe Cys
245 250 255

Asp Leu Phe Thr His Asp Glu Trp Ile Asn Tyr Asp Tyr Leu Gln Ser
260 265 270

Leu Lys Lys Tyr Tyr Gly His Gly Ala Gly Asn Pro Leu Gly Pro Thr
275 280 285

Gln Gly Val Gly Tyr Ala Asn Glu Leu Ile Ala Arg Leu Thr His Ser
290 295 300

Pro Val His Asp Asp Thr Ser Ser Asn His Thr Leu Asp Ser Ser Pro
305 310 315 320

Ala Thr Phe Pro Leu Asn Ser Thr Leu Tyr Ala Asp Phe Ser His Asp
325 330 335

Asn Gly Ile Ile Ser Ile Leu Phe Ala Leu Gly Leu Tyr Asn Gly Thr
340 345 350

Lys Pro Leu Ser Thr Thr Val Glu Asn Ile Thr Gln Thr Asp Gly
355 360 365

Phe Ser Ser Ala Trp Thr Val Pro Phe Ala Ser Arg Leu Tyr Val Glu
370 375 380

Met Met Gln Cys Gln Ala Glu Gln Glu Pro Leu Val Arg Val Leu Val
385 390 395 400

Asn Asp Arg Val Val Pro Leu His Gly Cys Pro Val Asp Ala Leu Gly
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35 40 45

Leu Val Gln Val Leu Ser Arg His Gly Ala Arg Tyr Pro Thr Ser Ser
50 55 60

Lys Ser Lys Lys Tyr Lys Lys Leu Val Thr Ala Ile Gln Ala Asn Ala
65 70 75 80

Thr Asp Phe Lys Gly Lys Phe Ala Phe Leu Lys Thr Tyr Asn Tyr Thr
85 90 95

Leu Gly Ala Asp Asp Leu Thr Pro Phe Gly Glu Gln Gln Leu Val Asn
100 105 110

Ser Gly Ile Lys Phe Tyr Gln Arg Tyr Lys Ala Leu Ala Arg Ser Val
115 120 125

Val Pro Phe Ile Arg Ala Ser Gly Ser Asp Arg Val Ile Ala Ser Gly
130 135 140

Glu Lys Phe Ile Glu Gly Phe Gln Gln Ala Lys Leu Ala Asp Pro Gly
145 150 155 160

Ala Thr Asn Arg Ala Ala Pro Ala Ile Ser Val Ile Ile Pro Glu Ser
165 170 175

Glu Thr Phe Asn Asn Thr Leu Asp His Gly Val Cys Thr Lys Phe Glu
180 185 190

Ala Ser Gln Leu Gly Asp Glu Val Ala Ala Asn Phe Thr Ala Leu Phe
195 200 205

Ala Pro Asp Ile Arg Ala Arg Ala Glu Lys His Leu Pro Gly Val Thr
210 215 220

Leu Thr Asp Glu Asp Val Val Ser Leu Met Asp Met Cys Ser Phe Asp
225 230 235 240

Thr Val Ala Arg Thr Ser Asp Ala Ser Gln Leu Ser Pro Phe Cys Gln
245 250 255

Leu Phe Thr His Asn Glu Trp Lys Lys Tyr Asn Tyr Leu Gln Ser Leu
260 265 270

Gly Lys Tyr Tyr Gly Tyr Gly Ala Gly Asn Pro Leu Gly Pro Ala Gln

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285

Gly Ile Gly Phe Thr Asn Glu Leu Ile Ala Arg Leu Thr Arg Ser Pro
290 295 300

Val Gln Asp His Thr Ser Thr Asn Ser Thr Leu Val Ser Asn Pro Ala
305 310 315 320

Thr Phe Pro Leu Asn Ala Thr Met Tyr Val Asp Phe Ser His Asp Asn
325 330 335

Ser Met Val Ser Ile Phe Phe Ala Leu Gly Leu Tyr Asn Gly Thr Glu
340 345 350

Pro Leu Ser Arg Thr Ser Val Glu Ser Ala Lys Glu Leu Asp Gly Tyr
355 360 365

Ser Ala Ser Trp Val Val Pro Phe Gly Ala Arg Ala Tyr Phe Glu Thr
370 375 380

Met Gln Cys Lys Ser Glu Lys Glu Pro Leu Val Arg Ala Leu Ile Asn
385 390 395 400

Asp Arg Val Val Pro Leu His Gly Cys Asp Val Asp Lys Leu Gly Arg
405 410 415

Cys Lys Leu Asn Asp Phe Val Lys Gly Leu Ser Trp Ala Arg Ser Gly
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Gly Asn Trp Gly Glu Cys Phe Ser
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35 40 45

Leu Val Gln Val Leu Ser Arg His Gly Ala Arg Tyr Pro Thr Ser Ser
50 55 60

Lys Ser Lys Lys Tyr Lys Lys Leu Val Thr Ala Ile Gln Ala Asn Ala
65 70 75 80

Thr Asp Phe Lys Gly Lys Phe Ala Phe Leu Lys Thr Tyr Asn Tyr Thr
85 90 95

Leu Gly Ala Asp Asp Leu Thr Pro Phe Gly Glu Gln Gln Leu Val Asn
100 105 110

Ser Gly Ile Lys Phe Tyr Gln Arg Tyr Lys Ala Leu Ala Arg Ser Val
115 120 125

Val Pro Phe Ile Arg Ala Ser Gly Ser Asp Arg Val Ile Ala Ser Gly
130 135 140

Glu Lys Phe Ile Glu Gly Phe Gln Gln Ala Lys Leu Ala Asp Pro Gly
145 150 155 160

Ala Thr Asn Arg Ala Ala Pro Ala Ile Ser Val Ile Ile Pro Glu Ser
165 170 175

Glu Thr Phe Asn Asn Thr Leu Asp His Gly Val Cys Thr Lys Phe Glu
180 185 190

Ala Ser Gln Leu Gly Asp Glu Val Ala Ala Asn Phe Thr Ala Leu Phe
195 200 205

Ala Pro Asp Ile Arg Ala Arg Ala Glu Lys His Leu Pro Gly Val Thr
210 215 220

Leu Thr Asp Glu Asp Val Val Ser Leu Met Asp Met Cys Ser Phe Asp
225 230 235 240

Thr Val Ala Arg Thr Ser Asp Ala Ser Gln Leu Ser Pro Phe Cys Gln
245 250 255

Leu Phe Thr His Asn Glu Trp Lys Lys Tyr Asn Tyr Leu Gln Ser Leu
260 265 270

Gly Lys Tyr Tyr Gly Tyr Gly Ala Gly Asn Pro Leu Gly Pro Ala Gln
275 280 285

Gly Ile Gly Phe Thr Asn Glu Leu Ile Ala Arg Leu Thr Arg Ser Pro
290 295 300

Val Gln Asp His Thr Ser Thr Asn Ser Thr Leu Val Ser Asn Pro Ala
305 310 315 320

Thr Phe Pro Leu Asn Ala Thr Met Tyr Val Asp Phe Ser His Asp Asn
325 330 335

Ser Met Val Ser Ile Phe Phe Ala Leu Gly Leu Tyr Asn Gly Thr Gly
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Pro Leu Ser Arg Thr Ser Val Glu Ser Ala Lys Glu Leu Asp Gly Tyr
355 360 365

Ser Ala Ser Trp Val Val Pro Phe Gly Ala Arg Ala Tyr Phe Glu Thr
370 375 380

Met Gln Cys Lys Ser Glu Lys Glu Pro Leu Val Arg Ala Leu Ile Asn
385 390 395 400

Asp Arg Val Val Pro Leu His Gly Cys Asp Val Asp Lys Leu Gly Arg
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Gly Asn Trp Gly Glu Cys Phe Ser
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Leu Val Gln Val Leu Ser Arg His Gly Ala Arg Tyr Pro Thr Ser Ser
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Lys Ser Lys Lys Tyr Lys Lys Leu Val Thr Ala Ile Gln Ala Asn Ala
65 70 75 80

Thr Asp Phe Lys Gly Lys Phe Ala Phe Leu Lys Thr Tyr Asn Tyr Thr
85 90 95

Leu Gly Ala Asp Asp Leu Thr Pro Phe Gly Glu Gln Gln Leu Val Asn
100 105 110

Ser Gly Ile Lys Phe Tyr Gln Arg Tyr Lys Ala Leu Ala Arg Ser Val
115 120 125

Val Pro Phe Ile Arg Ala Ser Gly Ser Asp Arg Val Ile Ala Ser Gly
130 135 140

Glu Lys Phe Ile Glu Gly Phe Gln Gln Ala Lys Leu Ala Asp Pro Gly
145 150 155 160

Ala Thr Asn Arg Ala Ala Pro Ala Ile Ser Val Ile Ile Pro Glu Ser
165 170 175

Glu Thr Phe Asn Asn Thr Leu Asp His Gly Val Cys Thr Lys Phe Glu
180 185 190

Ala Ser Gln Leu Gly Asp Glu Val Ala Ala Asn Phe Thr Ala Leu Phe
195 200 205

Ala Pro Asp Ile Arg Ala Arg Ala Glu Lys His Leu Pro Gly Val Thr
210 215 220

Leu Thr Asp Glu Asp Val Val Ser Leu Met Asp Met Cys Ser Phe Asp
225 230 235 240

Thr Val Ala Arg Thr Ser Asp Ala Ser Gln Leu Ser Pro Phe Cys Gln
245 250 255

Leu Phe Thr His Asn Glu Trp Lys Lys Tyr Asn Tyr Leu Gln Ser Leu
260 265 270

Gly Lys Tyr Tyr Gly Tyr Gly Ala Gly Asn Pro Leu Gly Pro Ala Gln
275 280 285

Gly Ile Gly Phe Thr Asn Glu Leu Ile Ala Arg Leu Thr Arg Ser Pro
290 295 300

Val Gln Asp His Thr Ser Thr Asn Ser Thr Leu Val Ser Asn Pro Ala
305 310 320

Thr Phe Pro Leu Asn Ala Thr Met Tyr Val Asp Phe Ser His Asp Asn
325 330 335

Ser Met Val Ser Ile Phe Phe Ala Leu Gly Leu Tyr Asn Gly Thr Glu
340 345 350

Pro Leu Ser Arg Thr Ser Val Glu Ser Ala Lys Glu Leu Asp Gly Tyr
355 360 365

Ser Ala Ser Trp Val Val Pro Phe Gly Ala Arg Ala Tyr Phe Glu Thr
370 375 380

Met Gln Cys Lys Ser Glu Lys Glu Ser Leu Val Arg Ala Leu Ile Asn
385 390 395 400

Asp Arg Val Val Pro Leu His Gly Cys Asp Val Asp Lys Leu Gly Arg
405 410 415

Cys Lys Leu Asn Asp Phe Val Lys Gly Leu Ser Trp Ala Arg Ser Gly
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Gly Asn Trp Gly Glu Cys Phe Ser
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20 25 30

Asp Glu Leu Ser Val Ser Ser Lys Leu Pro Lys Asp Cys Arg Ile Thr
35 40 45

Leu Val Gln Val Leu Ser Arg His Gly Ala Arg Tyr Pro Thr Ser Ser
50 55 60

Lys Ser Lys Lys Tyr Lys Leu Val Thr Ala Ile Gln Ala Asn Ala
65 70 75 80

Thr Asp Phe Lys Gly Lys Phe Ala Phe Leu Lys Thr Tyr Asn Tyr Thr
85 90 95

Leu Gly Ala Asp Asp Leu Thr Ala Phe Gly Glu Gln Gln Leu Val Asn
100 105 110

Ser Gly Ile Lys Phe Tyr Gln Arg Tyr Lys Ala Leu Ala Arg Ser Val
115 120 125

Val Pro Phe Ile Arg Ala Ser Gly Ser Asp Arg Val Ile Ala Ser Gly
130 135 140

Glu Lys Phe Ile Glu Gly Phe Gln Gln Ala Lys Leu Ala Asp Pro Gly
145 150 155 160

Ala Thr Asn Arg Ala Ala Pro Ala Ile Ser Val Ile Ile Pro Glu Ser
165 170 175

Glu Thr Phe Asn Asn Thr Leu Asp His Gly Val Cys Thr Lys Phe Glu
180 185 190

Ala Ser Gln Leu Gly Asp Glu Val Ala Ala Asn Phe Thr Ala Leu Phe
195 200 205

Ala Pro Asp Ile Arg Ala Arg Ala Lys Lys His Leu Pro Gly Val Thr
210 215 220

Leu Thr Asp Glu Asp Val Val Ser Leu Met Asp Met Cys Ser Phe Asp
225 230 235 240

Thr Val Ala Arg Thr Ser Asp Ala Ser Gln Leu Ser Pro Phe Cys Gln
245 250 255

Leu Phe Thr His Asn Glu Trp Lys Lys Tyr Asn Tyr Leu Gln Ser Leu
260 265 270

Gly Lys Tyr Tyr Gly Tyr Gly Ala Gly Asn Pro Leu Gly Pro Ala Gln
275 280 285

Gly Ile Gly Phe Thr Asn Glu Leu Ile Ala Arg Leu Thr Arg Ser Pro
290 295 300

Val Gln Asp His Thr Ser Thr Asn Ser Thr Leu Val Ser Asn Pro Ala
305 310 315 320

Thr Phe Pro Leu Asn Ala Thr Met Tyr Val Asp Phe Ser His Asp Asn
325 330 335

Ser Met Val Ser Ile Phe Phe Ala Leu Gly Leu Tyr Asn Gly Thr Glu
340 345 350

Pro Leu Ser Arg Thr Ser Val Glu Ser Ala Lys Glu Leu Asp Gly Tyr
355 360 365

Ser Ala Ser Trp Val Val Pro Phe Gly Ala Arg Ala Tyr Phe Glu Thr
370 375 380

Met Gln Cys Lys Ser Glu Lys Glu Pro Leu Val Arg Ala Leu Ile Asn
385 390 395 400

Asp Arg Val Val Pro Leu His Gly Cys Asp Val Asp Lys Leu Gly Arg
405 410 415

Cys Lys Leu Asn Asp Phe Val Lys Gly Leu Ser Trp Ala Arg Ser Gly
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Gly Asn Trp Gly Glu Cys Phe Ser
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Gly Thr Ser His Leu Trp Gly Gln Tyr Ser Pro Phe Phe Ser Leu Glu
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Asp Glu Leu Ser Val Ser Ser Asp Leu Pro Lys Asp Cys Arg Val Thr
35 40 45

Phe Val Gln Val Leu Ser Arg His Gly Ala Arg Tyr Pro Thr Ala Ser
50 55 60

Lys Ser Lys Lys Tyr Lys Lys Leu Val Thr Ala Ile Gln Lys Asn Ala
65 70 75 80

Thr Glu Phe Lys Gly Lys Phe Ala Phe Leu Glu Thr Tyr Asn Tyr Thr
85 90 95

Leu Gly Ala Asp Asp Leu Thr Pro Phe Gly Glu Gln Gln Met Val Asn
100 105 110

Ser Gly Ile Lys Phe Tyr Gln Lys Tyr Lys Ala Leu Ala Gly Ser Val
115 120 125

Val Pro Phe Ile Arg Ser Ser Gly Ser Asp Arg Val Ile Ala Ser Gly
130 135 140

Glu Lys Phe Ile Glu Gly Phe Gln Gln Ala Asn Val Ala Asp Pro Gly
145 150 155 160

Ala Thr Asn Arg Ala Ala Pro Val Ile Ser Val Ile Ile Pro Glu Ser
165 170 175

Glu Thr Tyr Asn Asn Thr Leu Asp His Ser Val Cys Thr Asn Phe Glu
180 185 190

Ala Ser Glu Leu Gly Asp Glu Val Glu Ala Asn Phe Thr Ala Leu Phe

195

200

205

Ala Pro Ala Ile Arg Ala Arg Ile Glu Lys His Leu Pro Gly Val Gln
210 215 220

Leu Thr Asp Asp Asp Val Val Ser Leu Met Asp Met Cys Ser Phe Asp
225 230 235 240

Thr Val Ala Arg Thr Ala Asp Ala Ser Glu Leu Ser Pro Phe Cys Ala
245 250 255

Ile Phe Thr His Asn Glu Trp Lys Lys Tyr Asp Tyr Leu Gln Ser Leu
260 265 270

Gly Lys Tyr Tyr Gly Tyr Gly Ala Gly Asn Pro Leu Gly Pro Ala Gln
275 280 285

Gly Ile Gly Phe Thr Asn Glu Leu Ile Ala Arg Leu Thr Asn Ser Pro
290 295 300

Val Gln Asp His Thr Ser Thr Asn Ser Thr Leu Asp Ser Asp Pro Ala
305 310 315 320

Thr Phe Pro Leu Asn Ala Thr Ile Tyr Val Asp Phe Ser His Asp Asn
325 330 335

Gly Met Ile Pro Ile Phe Phe Ala Met Gly Leu Tyr Asn Gly Thr Glu
340 345 350

Pro Leu Ser Gln Thr Ser Glu Glu Ser Thr Lys Glu Ser Asn Gly Tyr
355 360 365

Ser Ala Ser Trp Ala Val Pro Phe Gly Ala Arg Ala Tyr Phe Glu Thr
370 375 380

Met Gln Cys Lys Ser Glu Lys Glu Pro Leu Val Arg Ala Leu Ile Asn
385 390 395 400

Asp Arg Val Val Pro Leu His Gly Cys Ala Val Asp Lys Leu Gly Arg
405 410 415

Cys Lys Leu Lys Asp Phe Val Lys Gly Leu Ser Trp Ala Arg Ser Gly
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Gly Asn Ser Glu Gln Ser Phe Ser
435 440

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<400> 11

Gln Asn His Ser Cys Asn Thr Ala Asp Gly Gly Tyr Gln Cys Phe Pro
1 5 10 15

Asn Val Ser His Val Trp Gly Gln Tyr Ser Pro Tyr Phe Ser Ile Glu
20 25 30

Gln Glu Ser Ala Ile Ser Glu Asp Val Pro His Gly Cys Glu Val Thr
35 40 45

Phe Val Gln Val Leu Ser Arg His Gly Ala Arg Tyr Pro Thr Glu Ser
50 55 60

Lys Ser Lys Ala Tyr Ser Gly Leu Ile Glu Ala Ile Gln Lys Asn Ala
65 70 75 80

Thr Ser Phe Trp Gly Gln Tyr Ala Phe Leu Glu Ser Tyr Asn Tyr Thr
85 90 95

Leu Gly Ala Asp Asp Leu Thr Ile Phe Gly Glu Asn Gln Met Val Asp
100 105 110

Ser Gly Ala Lys Phe Tyr Arg Arg Tyr Lys Asn Leu Ala Arg Lys Asn
115 120 125

Thr Pro Phe Ile Arg Ala Ser Gly Ser Asp Arg Val Val Ala Ser Ala
130 135 140

Glu Lys Phe Ile Asn Gly Phe Arg Lys Ala Gln Leu His Asp His Gly
145 150 155 160

Ser Gly Gln Ala Thr Pro Val Val Asn Val Ile Ile Pro Glu Ile Asp
165 170 175

Gly Phe Asn Asn Thr Leu Asp His Ser Thr Cys Val Ser Phe Glu Asn
180 185 190

Asp Glu Arg Ala Asp Glu Ile Glu Ala Asn Phe Thr Ala Ile Met Gly
195 200 205

Pro Pro Ile Arg Lys Arg Leu Glu Asn Asp Leu Pro Gly Ile Lys Leu
210 215 220

Thr Asn Glu Asn Val Ile Tyr Leu Met Asp Met Cys Ser Phe Asp Thr
225 230 235 240

Met Ala Arg Thr Ala His Gly Thr Glu Leu Ser Pro Phe Cys Ala Ile
245 250 255

Phe Thr Glu Lys Glu Trp Leu Gln Tyr Asp Tyr Leu Gln Ser Leu Ser
260 265 270

Lys Tyr Tyr Gly Tyr Gly Ala Gly Ser Pro Leu Gly Pro Ala Gln Gly
275 280 285

Ile Gly Phe Thr Asn Glu Leu Ile Ala Arg Leu Thr Gln Ser Pro Val
290 295 300

Gln Asp Asn Thr Ser Thr Asn His Thr Leu Asp Ser Asn Pro Ala Thr
305 310 315 320

Phe Pro Leu Asp Arg Lys Leu Tyr Ala Asp Phe Ser His Asp Asn Ser
325 330 335

Met Ile Ser Ile Phe Phe Ala Met Gly Leu Tyr Asn Gly Thr Gln Pro
340 345 350

Leu Ser Met Asp Ser Val Glu Ser Ile Gln Glu Met Asp Gly Tyr Ala
355 360 365

Ala Ser Trp Thr Val Pro Phe Gly Ala Arg Ala Tyr Phe Glu Leu Met
370 375 380

Gln Cys Glu Lys Lys Glu Pro Leu Val Arg Val Leu Val Asn Asp Arg
385 390 395 400

Val Val Pro Leu His Gly Cys Ala Val Asp Lys Phe Gly Arg Cys Thr

405

410

415

Leu Asp Asp Trp Val Glu Gly Leu Asn Phe Ala Arg Ser Gly Gly Asn
420 425 430

Trp Lys Thr Cys Phe Thr Leu
435

<210> 12
<211> 443
<212> PRT
<213> Talaromyces Thermophilus

<400> 12

Asp Ser His Ser Cys Asn Thr Val Glu Gly Gly Tyr Gln Cys Arg Pro
1 5 10 15

Glu Ile Ser His Ser Trp Gly Gln Tyr Ser Pro Phe Phe Ser Leu Ala
20 25 30

Asp Gln Ser Glu Ile Ser Pro Asp Val Pro Gln Asn Cys Lys Ile Thr
35 40 45

Phe Val Gln Leu Leu Ser Arg His Gly Ala Arg Tyr Pro Thr Ser Ser
50 55 60

Lys Thr Glu Leu Tyr Ser Gln Leu Ile Ser Arg Ile Gln Lys Thr Ala
65 70 75 80

Thr Ala Tyr Lys Gly Tyr Tyr Ala Phe Leu Lys Asp Tyr Arg Tyr Gln
85 90 95

Leu Gly Ala Asn Asp Leu Thr Pro Phe Gly Glu Asn Gln Met Ile Gln
100 105 110

Leu Gly Ile Lys Phe Tyr Asn His Tyr Lys Ser Leu Ala Arg Asn Ala
115 120 125

Val Pro Phe Val Arg Cys Ser Gly Ser Asp Arg Val Ile Ala Ser Gly
130 135 140

Arg Leu Phe Ile Glu Gly Phe Gln Ser Ala Lys Val Leu Asp Pro His
145 150 155 160

Ser Asp Lys His Asp Ala Pro Pro Thr Ile Asn Val Ile Ile Glu Glu
165 170 175

Gly Pro Ser Tyr Asn Asn Thr Leu Asp Thr Gly Ser Cys Pro Val Phe
180 185 190

Glu Asp Ser Ser Gly Gly His Asp Ala Gln Glu Lys Phe Ala Lys Gln
195 200 205

Phe Ala Pro Ala Ile Leu Glu Lys Ile Lys Asp His Leu Pro Gly Val
210 215 220

Asp Leu Ala Val Ser Asp Val Pro Tyr Leu Met Asp Leu Cys Pro Phe
225 230 235 240

Glu Thr Leu Ala Arg Asn His Thr Asp Thr Leu Ser Pro Phe Cys Ala
245 250 255

Leu Ser Thr Gln Glu Glu Trp Gln Ala Tyr Asp Tyr Tyr Gln Ser Leu
260 265 270

Gly Lys Tyr Tyr Gly Asn Gly Gly Asn Pro Leu Gly Pro Ala Gln
275 280 285

Gly Val Gly Phe Val Asn Glu Leu Ile Ala Arg Met Thr His Ser Pro
290 295 300

Val Gln Asp Tyr Thr Val Asn His Thr Leu Asp Ser Asn Pro Ala
305 310 315 320

Thr Phe Pro Leu Asn Ala Thr Leu Tyr Ala Asp Phe Ser His Asp Asn
325 330 335

Thr Met Thr Ser Ile Phe Ala Ala Leu Gly Leu Tyr Asn Gly Thr Ala
340 345 350

Lys Leu Ser Thr Thr Glu Ile Lys Ser Ile Glu Glu Thr Asp Gly Tyr
355 360 365

Ser Ala Ala Trp Thr Val Pro Phe Gly Gly Arg Ala Tyr Ile Glu Met
370 375 380

Met Gln Cys Asp Asp Ser Asp Glu Pro Val Val Arg Val Leu Val Asn
385 390 395 400

Asp Arg Val Val Pro Leu His Gly Cys Glu Val Asp Ser Leu Gly Arg
405 410 415

Cys Lys Arg Asp Asp Phe Val Arg Gly Leu Ser Phe Ala Arg Gln Gly
420 425 430

Gly Asn Trp Glu Gly Cys Tyr Ala Ala Ser Glu
435 440

<210> 13
<211> 466
<212> PRT
<213> Myceliophthora thermophila

<400> 13

Glu Ser Arg Pro Cys Asp Thr Pro Asp Leu Gly Phe Gln Cys Gly Thr
1 5 10 15

Ala Ile Ser His Phe Trp Gly Gln Tyr Ser Pro Tyr Phe Ser Val Pro
20 25 30

Ser Glu Leu Asp Ala Ser Ile Pro Asp Asp Cys Glu Val Thr Phe Ala
35 40 45

Gln Val Leu Ser Arg His Gly Ala Arg Ala Pro Thr Leu Lys Arg Ala
50 55 60

Ala Ser Tyr Val Asp Leu Ile Asp Arg Ile His His Gly Ala Ile Ser
65 70 75 80

Tyr Gly Pro Gly Tyr Glu Phe Leu Arg Thr Tyr Asp Tyr Thr Leu Gly
85 90 95

Ala Asp Glu Leu Thr Arg Thr Gly Gln Gln Met Val Asn Ser Gly
100 105 110

Ile Lys Phe Tyr Arg Arg Tyr Arg Ala Leu Ala Arg Lys Ser Ile Pro
115 120 125

Phe Val Arg Thr Ala Gly Gln Asp Arg Val Val His Ser Ala Glu Asn
130 135 140

Phe Thr Gln Gly Phe His Ser Ala Leu Leu Ala Asp Arg Gly Ser Thr
145 150 155 160

Val Arg Pro Thr Leu Pro Tyr Asp Met Val Val Ile Pro Glu Thr Ala
165 170 175

Gly Ala Asn Asn Thr Leu His Asn Asp Leu Cys Thr Ala Phe Glu Glu
180 185 190

Gly Pro Tyr Ser Thr Ile Gly Asp Asp Ala Gln Asp Thr Tyr Leu Ser
195 200 205

Thr Phe Ala Gly Pro Ile Thr Ala Arg Val Asn Ala Asn Leu Pro Gly
210 215 220

Ala Asn Leu Thr Asp Ala Asp Thr Val Ala Leu Met Asp Leu Cys Pro
225 230 235 240

Phe Glu Thr Val Ala Ser Ser Ser Asp Pro Ala Thr Ala Asp Ala
245 250 255

Gly Gly Gly Asn Gly Arg Pro Leu Ser Pro Phe Cys Arg Leu Phe Ser
260 265 270

Glu Ser Glu Trp Arg Ala Tyr Asp Tyr Leu Gln Ser Val Gly Lys Trp
275 280 285

Tyr Gly Tyr Gly Pro Gly Asn Pro Leu Gly Pro Thr Gln Gly Val Gly
290 295 300

Phe Val Asn Glu Leu Leu Ala Arg Leu Ala Gly Val Pro Val Arg Asp
305 310 315 320

Gly Thr Ser Thr Asn Arg Thr Leu Asp Gly Asp Pro Arg Thr Phe Pro
325 330 335

Leu Gly Arg Pro Leu Tyr Ala Asp Phe Ser His Asp Asn Asp Met Met
340 345 350

Gly Val Leu Gly Ala Leu Gly Ala Tyr Asp Gly Val Pro Pro Leu Asp
355 360 365

Lys Thr Ala Arg Arg Asp Pro Glu Glu Leu Gly Gly Tyr Ala Ala Ser
370 375 380

Trp Ala Val Pro Phe Ala Ala Arg Ile Tyr Val Glu Lys Met Arg Cys
385 390 395 400

Ser Gly Gly Gly Gly Gly Gly Gly Glu Gly Arg Gln Glu Lys
405 410 415

Asp Glu Glu Met Val Arg Val Leu Val Asn Asp Arg Val Met Thr Leu
420 425 430

Lys Gly Cys Gly Ala Asp Glu Arg Gly Met Cys Thr Leu Glu Arg Phe
435 440 445

Ile Glu Ser Met Ala Phe Ala Arg Gly Asn Gly Lys Trp Asp Leu Cys
450 455 460

Phe Ala
465

<210> 14
<211> 441
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 14

Asn Ser His Ser Cys Asp Thr Val Asp Gly Gly Tyr Gln Cys Phe Pro
1 5 10 15

Glu Ile Ser His Leu Trp Gly Gln Tyr Ser Pro Tyr Phe Ser Leu Glu
20 25 30

Asp Glu Ser Ala Ile Ser Pro Asp Val Pro Asp Asp Cys Arg Val Thr
35 40 45

Phe Val Gln Val Leu Ser Arg His Gly Ala Arg Tyr Pro Thr Ser Ser
50 55 60

Lys Ser Lys Ala Tyr Ser Ala Leu Ile Glu Ala Ile Gln Lys Asn Ala
65 70 75 80

Thr Ala Phe Lys Gly Lys Tyr Ala Phe Leu Lys Thr Tyr Asn Tyr Thr
85 90 95

Leu Gly Ala Asp Asp Leu Thr Pro Phe Gly Glu Asn Gln Met Val Asn
100 105 110

Ser Gly Ile Lys Phe Tyr Arg Arg Tyr Lys Ala Leu Ala Arg Lys Ile
115 120 125

Val Pro Phe Ile Arg Ala Ser Gly Ser Asp Arg Val Ile Ala Ser Ala
130 135 140

Glu Lys Phe Ile Glu Gly Phe Gln Ser Ala Lys Leu Ala Asp Pro Gly
145 150 155 160

Ser Gln Pro His Gln Ala Ser Pro Val Ile Asp Val Ile Ile Pro Glu
165 170 175

Gly Ser Gly Tyr Asn Asn Thr Leu Asp His Gly Thr Cys Thr Ala Phe
180 185 190

Glu Asp Ser Glu Leu Gly Asp Asp Val Glu Ala Asn Phe Thr Ala Leu
195 200 205

Phe Ala Pro Ala Ile Arg Ala Arg Leu Glu Ala Asp Leu Pro Gly Val
210 215 220

Thr Leu Thr Asp Glu Asp Val Val Tyr Leu Met Asp Met Cys Pro Phe
225 230 235 240

Glu Thr Val Ala Arg Thr Ser Asp Ala Thr Glu Leu Ser Pro Phe Cys
245 250 255

Ala Leu Phe Thr His Asp Glu Trp Arg Gln Tyr Asp Tyr Leu Gln Ser
260 265 270

Leu Gly Lys Tyr Tyr Gly Ala Gly Asn Pro Leu Gly Pro Ala
275 280 285

Gln Gly Val Gly Phe Ala Asn Glu Leu Ile Ala Arg Leu Thr Arg Ser
290 295 300

Pro Val Gln Asp His Thr Ser Thr Asn His Thr Leu Asp Ser Asn Pro
305 310 315 320

Ala Thr Phe Pro Leu Asn Ala Thr Leu Tyr Ala Asp Phe Ser His Asp
325 330 335

Asn Ser Met Ile Ser Ile Phe Phe Ala Leu Gly Leu Tyr Asn Gly Thr
340 345 350

Ala Pro Leu Ser Thr Thr Ser Val Glu Ser Ile Glu Glu Thr Asp Gly
355 360 365

Tyr Ser Ala Ser Trp Thr Val Pro Phe Gly Ala Arg Ala Tyr Val Glu
370 375 380

Met Met Gln Cys Gln Ala Glu Lys Glu Pro Leu Val Arg Val Leu Val
385 390 395 400

Asn Asp Arg Val Val Pro Leu His Gly Cys Ala Val Asp Lys Leu Gly
405 410 415

Arg Cys Lys Arg Asp Asp Phe Val Glu Gly Leu Ser Phe Ala Arg Ser
420 425 430

Gly Gly Asn Trp Ala Glu Cys Phe Ala
435 440

<210> 15
<211> 1426
<212> DNA
<213> Artificial Sequence

<220>
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<220>
<221> CDS
<222> (12) .. (1412)
<223>

<220>
<221> sig_peptide
<222> (12) .. (89)
<223>

<220>
<221> mat_peptide

<222> (90) . . ()

<223>

<400> 15

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Met Gly Val Phe Val Val Leu Leu Ser Ile Ala Thr Leu
-25 -20 -15

ttc ggt tcc aca tcc ggt acc gcc ttg ggt cct cgt ggt aat tct cac 98
Phe Gly Ser Thr Ser Gly Thr Ala Leu Gly Pro Arg Gly Asn Ser His
-10 -5 -1 1

tct tgt gac act gtt gac ggt ggt tac caa tgt ttc cca gaa att tct 146
Ser Cys Asp Thr Val Asp Gly Gly Tyr Gln Cys Phe Pro Glu Ile Ser
5 10 15

cac ttg tgg ggt caa tac tct cca tac ttc tct ttg gaa gac gaa tct 194
His Leu Trp Gly Gln Tyr Ser Pro Tyr Phe Ser Leu Glu Asp Glu Ser
20 25 30 35

gct att tct cca gac gtt cca gac gac tgt aga gtt act ttc gtt caa 242
Ala Ile Ser Pro Asp Val Pro Asp Asp Cys Arg Val Thr Phe Val Gln
40 45 50

gtt ttg tct aga cac ggt gct aga tac cca act tct tct aag tct aag 290
Val Leu Ser Arg His Gly Ala Arg Tyr Pro Thr Ser Ser Lys Ser Lys
55 60 65

gct tac tct gct ttg att gaa gct att caa aag aac gct act gct ttc 338
Ala Tyr Ser Ala Leu Ile Glu Ala Ile Gln Lys Asn Ala Thr Ala Phe
70 75 80

aag ggt aag tac gct ttc ttg aag act tac aac tac act ttg ggt gct 386
Lys Gly Lys Tyr Ala Phe Leu Lys Thr Tyr Asn Tyr Thr Leu Gly Ala
85 90 95

gac gac ttg act cca ttc ggt gaa aac caa atg gtt aac tct ggt att 434
Asp Asp Leu Thr Pro Phe Gly Glu Asn Gln Met Val Asn Ser Gly Ile
100 105 110 115

aag ttc tac aga aga tac aag gct ttg gct aga aag att gtt cca ttc 482
Lys Phe Tyr Arg Arg Tyr Lys Ala Leu Ala Arg Lys Ile Val Pro Phe
120 125 130

att aga gct tct ggt tct gac aga gtt att gct tct gct gaa aag ttc 530
Ile Arg Ala Ser Gly Ser Asp Arg Val Ile Ala Ser Ala Glu Lys Phe
135 140 145

att gaa ggt ttc caa tct gct aag ttg gct gac cca ggt tct caa cca 578
Ile Glu Gly Phe Gln Ser Ala Lys Leu Ala Asp Pro Gly Ser Gln Pro
150 155 160

cac caa gct tct cca gtt att gac gtt att att cca gaa gga tcc ggt 626
His Gln Ala Ser Pro Val Ile Asp Val Ile Ile Pro Glu Gly Ser Gly
165 170 175

tac aac aac act ttg gac cac ggt act tgt act gct ttc gaa gac tct 674

Tyr Asn Asn Thr Leu Asp His Gly Thr Cys Thr Ala Phe Glu Asp Ser			
180	185	190	195
gaa ttg ggt gac gac gtt gaa gct aac ttc act gct ttg ttc gct cca			722
Glu Leu Gly Asp Asp Val Glu Ala Asn Phe Thr Ala Leu Phe Ala Pro			
200	205	210	
gct att aga gct aga ttg gaa gct gac ttg cca ggt gtt act ttg act			770
Ala Ile Arg Ala Arg Leu Glu Ala Asp Leu Pro Gly Val Thr Leu Thr			
215	220	225	
gac gaa gac gtt gtt tac ttg atg gac atg tgt cca ttc gaa act gtt			818
Asp Glu Asp Val Val Tyr Leu Met Asp Met Cys Pro Phe Glu Thr Val			
230	235	240	
gct aga act tct gac gct act gaa ttg tct cca ttc tgt gct ttg ttc			866
Ala Arg Thr Ser Asp Ala Thr Glu Leu Ser Pro Phe Cys Ala Leu Phe			
245	250	255	
act cac gac gaa tgg aga caa tac gac tac ttg caa tct ttg ggt aag			914
Thr His Asp Glu Trp Arg Gln Tyr Asp Tyr Leu Gln Ser Leu Gly Lys			
260	265	270	275
tac tac ggt tac ggt gct ggt aac cca ttg ggt cca gct caa ggt gtt			962
Tyr Tyr Gly Tyr Gly Ala Gly Asn Pro Leu Gly Pro Ala Gln Gly Val			
280	285	290	
ggt ttc gct aac gaa ttg att gct aga ttg act aga tct cca gtt caa			1010
Gly Phe Ala Asn Glu Leu Ile Ala Arg Leu Thr Arg Ser Pro Val Gln			
295	300	305	
gac cac act tct act aac cac act ttg gac tct aac cca gct act ttc			1058
Asp His Thr Ser Thr Asn His Thr Leu Asp Ser Asn Pro Ala Thr Phe			
310	315	320	
cca ttg aac gct act ttg tac gct gac ttc tct cac gac aac tct atg			1106
Pro Leu Asn Ala Thr Leu Tyr Ala Asp Phe Ser His Asp Asn Ser Met			
325	330	335	
att tct att ttc ttc gct ttg ggt ttg tac aac ggt act gct cca ttg			1154
Ile Ser Ile Phe Phe Ala Leu Gly Leu Tyr Asn Gly Thr Ala Pro Leu			
340	345	350	355
tct act act tct gtt gaa tct att gaa gaa act gac ggt tac tct gct			1202
Ser Thr Thr Ser Val Glu Ser Ile Glu Glu Thr Asp Gly Tyr Ser Ala			
360	365	370	
tct tgg act gtt cca ttc ggt gct aga gct tac gtt gaa atg atg caa			1250
Ser Trp Thr Val Pro Phe Gly Ala Arg Ala Tyr Val Glu Met Met Gln			
375	380	385	
tgt caa gct gaa aag gaa cca ttg gtt aga gtt ttg gtt aac gac aga			1298
Cys Gln Ala Glu Lys Glu Pro Leu Val Arg Val Leu Val Asn Asp Arg			
390	395	400	
gtt gtt cca ttg cac ggt tct gct gtt gac aag ttg ggt aga tct aag			1346
Val Val Pro Leu His Gly Cys Ala Val Asp Lys Leu Gly Arg Cys Lys			

405	410	415	
aga gac gac ttc gtt gaa ggt ttg tct ttc gct aga tct ggt ggt aac Arg Asp Asp Phe Val Glu Gly Leu Ser Phe Ala Arg Ser Gly Gly Asn			1394
420	425	430	435
tgg gct gaa tgt ttc gct taagaattca tata Trp Ala Glu Cys Phe Ala			1426
440			
<210> 16			
<211> 467			
<212> PRT			
<213> Artificial Sequence			
<220>			
<223> Synthetic			
<400> 16			
Met Gly Val Phe Val Val Leu Leu Ser Ile Ala Thr Leu Phe Gly Ser			
-25	-20	-15	
Thr Ser Gly Thr Ala Leu Gly Pro Arg Gly Asn Ser His Ser Cys Asp			
-10	-5	-1 1	5
Thr Val Asp Gly Gly Tyr Gln Cys Phe Pro Glu Ile Ser His Leu Trp			
10	15	20	
Gly Gln Tyr Ser Pro Tyr Phe Ser Leu Glu Asp Glu Ser Ala Ile Ser			
25	30	35	
Pro Asp Val Pro Asp Asp Cys Arg Val Thr Phe Val Gln Val Leu Ser			
40	45	50	
Arg His Gly Ala Arg Tyr Pro Thr Ser Ser Lys Ser Lys Ala Tyr Ser			
55	60	65	70
Ala Leu Ile Glu Ala Ile Gln Lys Asn Ala Thr Ala Phe Lys Gly Lys			
75	80	85	
Tyr Ala Phe Leu Lys Thr Tyr Asn Tyr Thr Leu Gly Ala Asp Asp Leu			
90	95	100	
Thr Pro Phe Gly Glu Asn Gln Met Val Asn Ser Gly Ile Lys Phe Tyr			
105	110	115	

Arg Arg Tyr Lys Ala Leu Ala Arg Lys Ile Val Pro Phe Ile Arg Ala
120 125 130

Ser Gly Ser Asp Arg Val Ile Ala Ser Ala Glu Lys Phe Ile Glu Gly
135 140 145 150

Phe Gln Ser Ala Lys Leu Ala Asp Pro Gly Ser Gln Pro His Gln Ala
155 160 165

Ser Pro Val Ile Asp Val Ile Ile Pro Glu Gly Ser Gly Tyr Asn Asn
170 175 180

Thr Leu Asp His Gly Thr Cys Thr Ala Phe Glu Asp Ser Glu Leu Gly
185 190 195

Asp Asp Val Glu Ala Asn Phe Thr Ala Leu Phe Ala Pro Ala Ile Arg
200 205 210

Ala Arg Leu Glu Ala Asp Leu Pro Gly Val Thr Leu Thr Asp Glu Asp
215 220 225 230

Val Val Tyr Leu Met Asp Met Cys Pro Phe Glu Thr Val Ala Arg Thr
235 240 245

Ser Asp Ala Thr Glu Leu Ser Pro Phe Cys Ala Leu Phe Thr His Asp
250 255 260

Glu Trp Arg Gln Tyr Asp Tyr Leu Gln Ser Leu Gly Lys Tyr Tyr Gly
265 270 275

Tyr Gly Ala Gly Asn Pro Leu Gly Pro Ala Gln Gly Val Gly Phe Ala
280 285 290

Asn Glu Leu Ile Ala Arg Leu Thr Arg Ser Pro Val Gln Asp His Thr
295 300 305 310

Ser Thr Asn His Thr Leu Asp Ser Asn Pro Ala Thr Phe Pro Leu Asn
315 320 325

Ala Thr Leu Tyr Ala Asp Phe Ser His Asp Asn Ser Met Ile Ser Ile
330 335 340

Phe Phe Ala Leu Gly Leu Tyr Asn Gly Thr Ala Pro Leu Ser Thr Thr

345

350

355

Ser Val Glu Ser Ile Glu Glu Thr Asp Gly Tyr Ser Ala Ser Trp Thr
360 365 370

Val Pro Phe Gly Ala Arg Ala Tyr Val Glu Met Met Gln Cys Gln Ala
375 380 385 390

Glu Lys Glu Pro Leu Val Arg Val Leu Val Asn Asp Arg Val Val Pro
395 400 405

Leu His Gly Cys Ala Val Asp Lys Leu Gly Arg Cys Lys Arg Asp Asp
410 415 420

Phe Val Glu Gly Leu Ser Phe Ala Arg Ser Gly Gly Asn Trp Ala Glu
425 430 435

Cys Phe Ala
440

<210> 17
<211> 422
<212> PRT
<213> Paxillus involutus phyA1

<400> 17

Ser Val Pro Lys Asn Thr Ala Pro Thr Phe Pro Ile Pro Glu Ser Glu
1 5 10 15

Gln Arg Asn Trp Ser Pro Tyr Ser Pro Tyr Phe Pro Leu Ala Glu Tyr
20 25 30

Lys Ala Pro Pro Ala Gly Cys Gln Ile Asn Gln Val Asn Ile Ile Gln
35 40 45

Arg His Gly Ala Arg Phe Pro Thr Ser Gly Ala Thr Thr Arg Ile Lys
50 55 60

Ala Gly Leu Thr Lys Leu Gln Gly Val Gln Asn Phe Thr Asp Ala Lys
65 70 75 80

Phe Asn Phe Ile Lys Ser Phe Lys Tyr Asp Leu Gly Asn Ser Asp Leu
85 90 95

Val Pro Phe Gly Ala Ala Gln Ser Phe Asp Ala Gly Gln Glu Ala Phe
100 105 110

Ala Arg Tyr Ser Lys Leu Val Ser Lys Asn Asn Leu Pro Phe Ile Arg
115 120 125

Ala Asp Gly Ser Asp Arg Val Val Asp Ser Ala Thr Asn Trp Thr Ala
130 135 140

Gly Phe Ala Ser Ala Ser His Asn Thr Val Gln Pro Lys Leu Asn Leu
145 150 155 160

Ile Leu Pro Gln Thr Gly Asn Asp Thr Leu Glu Asp Asn Met Cys Pro
165 170 175

Ala Ala Gly Asp Ser Asp Pro Gln Val Asn Ala Trp Leu Ala Val Ala
180 185 190

Phe Pro Ser Ile Thr Ala Arg Leu Asn Ala Ala Pro Ser Val Asn
195 200 205

Leu Thr Asp Thr Asp Ala Phe Asn Leu Val Ser Leu Cys Ala Phe Leu
210 215 220

Thr Val Ser Lys Glu Lys Lys Ser Asp Phe Cys Thr Leu Phe Glu Gly
225 230 235 240

Ile Pro Gly Ser Phe Glu Ala Phe Ala Tyr Gly Gly Asp Leu Asp Lys
245 250 255

Phe Tyr Gly Thr Gly Tyr Gly Gln Glu Leu Gly Pro Val Gln Gly Val
260 265 270

Gly Tyr Val Asn Glu Leu Ile Ala Arg Leu Thr Asn Ser Ala Val Arg
275 280 285

Asp Asn Thr Gln Thr Asn Arg Thr Leu Asp Ala Ser Pro Val Thr Phe
290 295 300

Pro Leu Asn Lys Thr Phe Tyr Ala Asp Phe Ser His Asp Asn Leu Met
305 310 315 320

Val Ala Val Phe Ser Ala Met Gly Leu Phe Arg Gln Pro Ala Pro Leu
325 330 335

Ser Thr Ser Val Pro Asn Pro Trp Arg Thr Trp Arg Thr Ser Ser Leu
340 345 350

Val Pro Phe Ser Gly Arg Met Val Val Glu Arg Leu Ser Cys Phe Gly
355 360 365

Thr Thr Lys Val Arg Val Leu Val Gln Asp Gln Val Gln Pro Leu Glu
370 375 380

Phe Cys Gly Gly Asp Arg Asn Gly Leu Cys Thr Leu Ala Lys Phe Val
385 390 395 400

Glu Ser Gln Thr Phe Ala Arg Ser Asp Gly Ala Gly Asp Phe Glu Lys
405 410 415

Cys Phe Ala Thr Ser Ala
420

<210> 18
<211> 422
<212> PRT
<213> Paxillus involutus phyA2

<400> 18

Ser Val Pro Arg Asn Ile Ala Pro Lys Phe Ser Ile Pro Glu Ser Glu
1 5 10 15

Gln Arg Asn Trp Ser Pro Tyr Ser Pro Tyr Phe Pro Leu Ala Glu Tyr
20 25 30

Lys Ala Pro Pro Ala Gly Cys Glu Ile Asn Gln Val Asn Ile Ile Gln
35 40 45

Arg His Gly Ala Arg Phe Pro Thr Ser Gly Ala Ala Thr Arg Ile Lys
50 55 60 65

Ala Gly Leu Ser Lys Leu Gln Ser Val Gln Asn Phe Thr Asp Pro Lys
65 70 75 80

Phe Asp Phe Ile Lys Ser Phe Thr Tyr Asp Leu Gly Thr Ser Asp Leu
85 90 95

Val Pro Phe Gly Ala Ala Gln Ser Phe Asp Ala Gly Leu Glu Val Phe
100 105 110

Ala Arg Tyr Ser Lys Leu Val Ser Ser Asp Asn Leu Pro Phe Ile Arg
115 120 125

Ser Asp Gly Ser Asp Arg Val Val Asp Thr Ala Thr Asn Trp Thr Ala
130 135 140

Gly Phe Ala Ser Ala Ser Arg Asn Ala Ile Gln Pro Lys Leu Asp Leu
145 150 155 160

Ile Leu Pro Gln Thr Gly Asn Asp Thr Leu Glu Asp Asn Met Cys Pro
165 170 175

Ala Ala Gly Glu Ser Asp Pro Gln Val Asp Ala Trp Leu Ala Ser Ala
180 185 190

Phe Pro Ser Val Thr Ala Gln Leu Asn Ala Ala Pro Gly Ala Asn
195 200 205

Leu Thr Asp Ala Asp Ala Phe Asn Leu Val Ser Leu Cys Pro Phe Met
210 215 220

Thr Val Ser Lys Glu Gln Lys Ser Asp Phe Cys Thr Leu Phe Glu Gly
225 230 235 240

Ile Pro Gly Ser Phe Glu Ala Phe Ala Tyr Ala Gly Asp Leu Asp Lys
245 250 255

Phe Tyr Gly Thr Gly Tyr Gly Gln Ala Leu Gly Pro Val Gln Gly Val
260 265 270

Gly Tyr Ile Asn Glu Leu Leu Ala Arg Leu Thr Asn Ser Ala Val Asn
275 280 285

Asp Asn Thr Gln Thr Asn Arg Thr Leu Asp Ala Ala Pro Asp Thr Phe
290 295 300

Pro Leu Asn Lys Thr Met Tyr Ala Asp Phe Ser His Asp Asn Leu Met
305 310 315 320

Val Ala Val Phe Ser Ala Met Gly Leu Phe Arg Gln Ser Ala Pro Leu
325 330 335

Ser Thr Ser Thr Pro Asp Pro Asn Arg Thr Trp Leu Thr Ser Ser Val
340 345 350

Val Pro Phe Ser Ala Arg Met Ala Val Glu Arg Leu Ser Cys Ala Gly
355 360 365

Thr Thr Lys Val Arg Val Leu Val Gln Asp Gln Val Gln Pro Leu Glu
370 375 380

Phe Cys Gly Gly Asp Gln Asp Gly Leu Cys Ala Leu Asp Lys Phe Val
385 390 395 400

Glu Ser Gln Ala Tyr Ala Arg Ser Gly Gly Ala Gly Asp Phe Glu Lys
405 410 415

Cys Leu Ala Thr Thr Val
420

<210> 19
<211> 420
<212> PRT
<213> Trametes Pubescens

<400> 19

His Ile Pro Leu Arg Asp Thr Ser Ala Cys Leu Asp Val Thr Arg Asp
1 5 10 15

Val Gln Gln Ser Trp Ser Met Tyr Ser Pro Tyr Phe Pro Ala Ala Thr
20 25 30

Tyr Val Ala Pro Pro Ala Ser Cys Gln Ile Asn Gln Val His Ile Ile
35 40 45

Gln Arg His Gly Ala Arg Phe Pro Thr Ser Gly Ala Ala Lys Arg Ile
50 55 60

Gln Thr Ala Val Ala Lys Leu Lys Ala Ala Ser Asn Tyr Thr Asp Pro
65 70 75 80

Leu Leu Ala Phe Val Thr Asn Tyr Thr Tyr Ser Leu Gly Gln Asp Ser

85

90

95

Leu Val Glu Leu Gly Ala Thr Gln Ser Ser Glu Ala Gly Gln Glu Ala
100 105 110

Phe Thr Arg Tyr Ser Ser Leu Val Ser Ala Asp Glu Leu Pro Phe Val
115 120 125

Arg Ala Ser Gly Ser Asp Arg Val Val Ala Thr Ala Asn Asn Trp Thr
130 135 140

Ala Gly Phe Ala Leu Ala Ser Ser Asn Ser Ile Thr Pro Val Leu Ser
145 150 155 160

Val Ile Ile Ser Glu Ala Gly Asn Asp Thr Leu Asp Asp Asn Met Cys
165 170 175

Pro Ala Ala Gly Asp Ser Asp Pro Gln Val Asn Gln Trp Leu Ala Gln
180 185 190

Phe Ala Pro Pro Met Thr Ala Arg Leu Asn Ala Gly Ala Pro Gly Ala
195 200 205

Asn Leu Thr Asp Thr Asp Thr Tyr Asn Leu Leu Thr Leu Cys Pro Phe
210 215 220

Glu Thr Val Ala Thr Glu Arg Arg Ser Glu Phe Cys Asp Ile Tyr Glu
225 230 235 240

Glu Leu Gln Ala Glu Asp Ala Phe Ala Tyr Asn Ala Asp Leu Asp Lys
245 250 255

Phe Tyr Gly Thr Gly Tyr Gly Gln Pro Leu Gly Pro Val Gln Gly Val
260 265 270

Gly Tyr Ile Asn Glu Leu Ile Ala Arg Leu Thr Ala Gln Asn Val Ser
275 280 285

Asp His Thr Gln Thr Asn Ser Thr Leu Asp Ser Ser Pro Glu Thr Phe
290 295 300

Pro Leu Asn Arg Thr Leu Tyr Ala Asp Phe Ser His Asp Asn Gln Met
305 310 315 320

Val Ala Ile Phe Ser Ala Met Gly Leu Phe Asn Gln Ser Ala Pro Leu
325 330 335

Asp Pro Thr Thr Pro Asp Pro Ala Arg Thr Phe Leu Val Lys Lys Ile
340 345 350

Val Pro Phe Ser Ala Arg Met Val Val Glu Arg Leu Asp Cys Gly Gly
355 360 365

Ala Gln Ser Val Arg Leu Leu Val Asn Asp Ala Val Gln Pro Leu Ala
370 375 380

Phe Cys Gly Ala Asp Thr Ser Gly Val Cys Thr Leu Asp Ala Phe Val
385 390 395 400

Glu Ser Gln Ala Tyr Ala Arg Asn Asp Gly Glu Gly Asp Phe Glu Lys
405 410 415

Cys Phe Ala Thr
420

<210> 20
<211> 435
<212> PRT
<213> Agrocybe peidades

<400> 20

Gly Gly Val Val Gln Ala Thr Phe Val Gln Pro Phe Phe Pro Pro Gln
1 5 10 15

Ile Gln Asp Ser Trp Ala Ala Tyr Thr Pro Tyr Tyr Pro Val Gln Ala
20 25 30

Tyr Thr Pro Pro Pro Lys Asp Cys Lys Ile Thr Gln Val Asn Ile Ile
35 40 45

Gln Arg His Gly Ala Arg Phe Pro Thr Ser Gly Ala Gly Thr Arg Ile
50 55 60

Gln Ala Ala Val Lys Lys Leu Gln Ser Ala Lys Thr Tyr Thr Asp Pro
65 70 75 80

Arg Leu Asp Phe Leu Thr Asn Tyr Thr Tyr Thr Leu Gly His Asp Asp
85 90 95

Leu Val Pro Phe Gly Ala Leu Gln Ser Ser Gln Ala Gly Glu Glu Thr
100 105 110

Phe Gln Arg Tyr Ser Phe Leu Val Ser Lys Glu Asn Leu Pro Phe Val
115 120 125

Arg Ala Ser Ser Ser Asn Arg Val Val Asp Ser Ala Thr Asn Trp Thr
130 135 140

Glu Gly Phe Ser Ala Ala Ser His His Val Leu Asn Pro Ile Leu Phe
145 150 155 160

Val Ile Leu Ser Glu Ser Leu Asn Asp Thr Leu Asp Asp Ala Met Cys
165 170 175

Pro Asn Ala Gly Ser Ser Asp Pro Gln Thr Gly Ile Trp Thr Ser Ile
180 185 190

Tyr Gly Thr Pro Ile Ala Asn Arg Leu Asn Gln Gln Ala Pro Gly Ala
195 200 205

Asn Ile Thr Ala Ala Asp Val Ser Asn Leu Ile Pro Leu Cys Ala Phe
210 215 220

Glu Thr Ile Val Lys Glu Thr Pro Ser Pro Phe Cys Asn Leu Phe Thr
225 230 235 240

Pro Glu Glu Phe Ala Gln Phe Glu Tyr Phe Gly Asp Leu Asp Lys Phe
245 250 255

Tyr Gly Thr Gly Tyr Gly Gln Pro Leu Gly Pro Val Gln Gly Val Gly
260 265 270

Tyr Ile Asn Glu Leu Leu Ala Arg Leu Thr Glu Met Pro Val Arg Asp
275 280 285

Asn Thr Gln Thr Asn Arg Thr Leu Asp Ser Ser Pro Leu Thr Phe Pro
290 295 300

Leu Asp Arg Ser Ile Tyr Ala Asp Leu Ser His Asp Asn Gln Met Ile

305 310 315 320

Ala Ile Phe Ser Ala Met Gly Leu Phe Asn Gln Ser Ser Pro Leu Asp
325 330 335

Pro Ser Phe Pro Asn Pro Lys Arg Thr Trp Val Thr Ser Arg Leu Thr
340 345 350

Pro Phe Ser Ala Arg Met Val Thr Glu Arg Leu Leu Cys Gln Arg Asp
355 360 365

Gly Thr Gly Ser Gly Gly Pro Ser Arg Ile Met Arg Asn Gly Asn Val
370 375 380

Gln Thr Phe Val Arg Ile Leu Val Asn Asp Ala Leu Gln Pro Leu Lys
385 390 395 400

Phe Cys Gly Gly Asp Met Asp Ser Leu Cys Thr Leu Glu Ala Phe Val
405 410 415

Glu Ser Gln Lys Tyr Ala Arg Glu Asp Gly Gln Gly Asp Phe Glu Lys
420 425 430

Cys Phe Asp
435

<210> 21
<211> 419
<212> PRT
<213> Peniophora lycii

<400> 21

Ser Thr Gln Phe Ser Phe Val Ala Ala Gln Leu Pro Ile Pro Ala Gln
1 5 10 15

Asn Thr Ser Asn Trp Gly Pro Tyr Asp Pro Phe Phe Pro Val Glu Pro
20 25 30

Tyr Ala Ala Pro Pro Glu Gly Cys Thr Val Thr Gln Val Asn Leu Ile
35 40 45

Gln Arg His Gly Ala Arg Trp Pro Thr Ser Gly Ala Arg Ser Arg Gln
50 55 60

Val Ala Ala Val Ala Lys Ile Gln Met Ala Arg Pro Phe Thr Asp Pro
65 70 75 80

Lys Tyr Glu Phe Leu Asn Asp Phe Val Tyr Lys Phe Gly Val Ala Asp
85 90 95

Leu Leu Pro Phe Gly Ala Asn Gln Ser His Gln Thr Gly Thr Asp Met
100 105 110

Tyr Thr Arg Tyr Ser Thr Leu Phe Glu Gly Gly Asp Val Pro Phe Val
115 120 125

Arg Ala Ala Gly Asp Gln Arg Val Val Asp Ser Ser Thr Asn Trp Thr
130 135 140

Ala Gly Phe Gly Asp Ala Ser Gly Glu Thr Val Leu Pro Thr Leu Gln
145 150 155 160

Val Val Leu Gln Glu Glu Gly Asn Cys Thr Leu Cys Asn Asn Met Cys
165 170 175

Pro Asn Glu Val Asp Gly Asp Glu Ser Thr Thr Trp Leu Gly Val Phe
180 185 190

Ala Pro Asn Ile Thr Ala Arg Leu Asn Ala Ala Ala Pro Ser Ala Asn
195 200 205

Leu Ser Asp Ser Asp Ala Leu Thr Leu Met Asp Met Cys Pro Phe Asp
210 215 220

Thr Leu Ser Ser Gly Asn Ala Ser Pro Phe Cys Asp Leu Phe Thr Ala
225 230 235 240

Glu Glu Tyr Val Ser Tyr Glu Tyr Tyr Asp Leu Asp Lys Tyr Tyr
245 250 255

Gly Thr Gly Pro Gly Asn Ala Leu Gly Pro Val Gln Gly Val Gly Tyr
260 265 270

Val Asn Glu Leu Leu Ala Arg Leu Thr Gly Gln Ala Val Arg Asp Glu
275 280 285

Thr Gln Thr Asn Arg Thr Leu Asp Ser Asp Pro Ala Thr Phe Pro Leu
290 295 300

Asn Arg Thr Phe Tyr Ala Asp Phe Ser His Asp Asn Thr Met Val Pro
305 310 315 320

Ile Phe Ala Ala Leu Gly Leu Phe Asn Ala Thr Ala Leu Asp Pro Leu
325 330 335

Lys Pro Asp Glu Asn Arg Leu Trp Val Asp Ser Lys Leu Val Pro Phe
340 345 350

Ser Gly His Met Thr Val Glu Lys Leu Ala Cys Ser Gly Lys Glu Ala
355 360 365

Val Arg Val Leu Val Asn Asp Ala Val Gln Pro Leu Glu Phe Cys Gly
370 375 380

Gly Val Asp Gly Val Cys Glu Leu Ser Ala Phe Val Glu Ser Gln Thr
385 390 395 400

Tyr Ala Arg Glu Asn Gly Gln Gly Asp Phe Ala Lys Cys Gly Phe Val
405 410 415

Pro Ser Glu

<210> 22
<211> 369
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 22

Ser Pro Arg Thr Ala Ala Gln Leu Pro Ile Pro Gln Gln Trp Ser Pro
1 5 10 15

Tyr Ser Pro Tyr Phe Pro Val Ala Tyr Ala Pro Pro Ala Gly Cys Gln
20 25 30

Ile Gln Val Asn Ile Ile Gln Arg His Gly Ala Arg Phe Pro Thr Ser
35 40 45

Gly Ala Ala Thr Arg Ile Gln Ala Ala Val Ala Lys Leu Gln Ser Ala
50 55 60

Thr Asp Pro Lys Leu Asp Phe Leu Asn Thr Tyr Leu Gly Asp Asp Leu
65 70 75 80

Val Pro Phe Gly Ala Gln Ser Ser Gln Ala Gly Gln Glu Ala Phe Thr
85 90 95

Arg Tyr Ser Leu Val Ser Asp Asn Leu Pro Phe Val Arg Ala Ser Gly
100 105 110

Ser Asp Arg Val Val Asp Ser Ala Thr Asn Trp Thr Ala Gly Phe Ala
115 120 125

Ala Ser Asn Thr Pro Leu Val Ile Leu Ser Glu Gly Asn Asp Thr Leu
130 135 140

Asp Asp Asn Met Cys Pro Ala Gly Asp Ser Asp Pro Gln Asn Trp Leu
145 150 155 160

Ala Val Phe Ala Pro Pro Ile Thr Ala Arg Leu Asn Ala Ala Pro
165 170 175

Gly Ala Asn Leu Thr Asp Asp Ala Asn Leu Leu Cys Pro Phe Glu Thr
180 185 190

Val Ser Glu Ser Phe Cys Asp Leu Phe Glu Pro Glu Glu Phe Ala Phe
195 200 205

Tyr Gly Asp Leu Asp Lys Phe Tyr Gly Thr Gly Tyr Gly Gln Pro Leu
210 215 220

Gly Pro Val Gln Gly Val Gly Tyr Ile Asn Glu Leu Leu Ala Arg Leu
225 230 235 240

Thr Gln Ala Val Arg Asp Asn Thr Gln Thr Asn Arg Thr Leu Asp Ser
245 250 255

Ser Pro Thr Phe Pro Leu Asn Arg Thr Phe Tyr Ala Asp Phe Ser His
260 265 270

Asp Asn Gln Met Val Ala Ile Phe Ser Ala Met Gly Leu Phe Asn Gln
275 280 285

Ser Ala Pro Leu Asp Pro Ser Pro Asp Pro Asn Arg Thr Trp Val Thr
290 295 300

Ser Lys Leu Val Pro Phe Ser Ala Arg Met Val Val Glu Arg Leu Cys
305 310 315 320

Gly Thr Val Arg Val Leu Val Asn Asp Ala Val Gln Pro Leu Glu Phe
325 330 335

Cys Gly Gly Asp Asp Gly Cys Thr Leu Asp Ala Phe Val Glu Ser Gln
340 345 350

Tyr Ala Arg Glu Asp Gly Gln Gly Asp Phe Glu Lys Cys Phe Ala Thr
355 360 365

Pro

<210> 23
<211> 440
<212> PRT
<213> Thermomyces lanuginosus

<400> 23

Asn Val Asp Ile Ala Arg His Trp Gly Gln Tyr Ser Pro Phe Phe Ser
1 5 10 15

Leu Ala Glu Val Ser Glu Ile Ser Pro Ala Val Pro Lys Gly Cys Arg
20 25 30

Val Glu Phe Val Gln Val Leu Ser Arg His Gly Ala Arg Tyr Pro Thr
35 40 45

Ala His Lys Ser Glu Val Tyr Ala Glu Leu Leu Gln Arg Ile Gln Asp
50 55 60

Thr Ala Thr Glu Phe Lys Gly Asp Phe Ala Phe Leu Arg Asp Tyr Ala
65 70 75 80

Tyr His Leu Gly Ala Asp Asn Leu Thr Arg Phe Gly Glu Glu Gln Met
85 90 95

Met Glu Ser Gly Arg Gln Phe Tyr His Arg Tyr Arg Glu Gln Ala Arg
100 105 110

Glu Ile Val Pro Phe Val Arg Ala Ala Gly Ser Ala Arg Val Ile Ala
115 120 125

Ser Ala Glu Phe Phe Asn Arg Gly Phe Gln Asp Ala Lys Asp Arg Asp
130 135 140

Pro Arg Ser Asn Lys Asp Gln Ala Glu Pro Val Ile Asn Val Ile Ile
145 150 155 160

Ser Glu Glu Thr Gly Ser Asn Asn Thr Leu Asp Gly Leu Thr Cys Pro
165 170 175

Ala Ala Glu Glu Ala Pro Asp Pro Thr Gln Pro Ala Glu Phe Leu Gln
180 185 190

Val Phe Gly Pro Arg Val Leu Lys Lys Ile Thr Lys His Met Pro Gly
195 200 205

Val Asn Leu Thr Leu Glu Asp Val Pro Leu Phe Met Asp Leu Cys Pro
210 215 220

Phe Asp Thr Val Gly Ser Asp Pro Val Leu Phe Pro Arg Gln Leu Ser
225 230 235 240

Pro Phe Cys His Leu Phe Thr Ala Asp Asp Trp Met Ala Tyr Asp Tyr
245 250 255

Tyr Tyr Thr Leu Asp Lys Tyr Tyr Ser His Gly Gly Gly Ser Ala Phe
260 265 270

Gly Pro Ser Arg Gly Val Gly Phe Val Asn Glu Leu Ile Ala Arg Met
275 280 285

Thr Gly Asn Leu Pro Val Lys Asp His Thr Thr Val Asn His Thr Leu
290 295 300

Asp Asp Asn Pro Glu Thr Phe Pro Leu Asp Ala Val Leu Tyr Ala Asp
305 310 315 320

Phe Ser His Asp Asn Thr Met Thr Gly Ile Phe Ser Ala Met Gly Leu
325 330 335

Tyr Asn Gly Thr Lys Pro Leu Ser Thr Ser Lys Ile Gln Pro Pro Thr
340 345 350

Gly Ala Ala Ala Asp Gly Tyr Ala Ala Ser Trp Thr Val Pro Phe Ala
355 360 365

Ala Arg Ala Tyr Val Glu Leu Leu Arg Cys Glu Thr Glu Thr Ser Ser
370 375 380

Glu Glu Glu Glu Glu Gly Glu Asp Glu Pro Phe Val Arg Val Leu Val
385 390 400

Asn Asp Arg Val Val Pro Leu His Gly Cys Arg Val Asp Arg Trp Gly
405 410 415

Arg Cys Arg Arg Asp Glu Trp Ile Lys Gly Leu Thr Phe Ala Arg Gln
420 425 430

Gly Gly His Trp Asp Arg Cys Phe
435 440

<210> 24
<211> 441
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 24

Asn Ser His Ser Cys Asp Thr Val Asp Gly Gly Tyr Gln Cys Phe Pro
1 5 10 15

Glu Ile Ser His Leu Trp Gly Gln Tyr Ser Pro Phe Phe Ser Leu Ala
20 25 30

Asp Glu Ser Ala Ile Ser Pro Asp Val Pro Lys Gly Cys Arg Val Thr
35 40 45

Phe Val Gln Val Leu Ser Arg His Gly Ala Arg Tyr Pro Thr Ser Ser
50 55 60

Lys Ser Lys Lys Tyr Ser Ala Leu Ile Glu Ala Ile Gln Lys Asn Ala
65 70 75 80

Thr Ala Phe Lys Gly Lys Tyr Ala Phe Leu Lys Thr Tyr Asn Tyr Thr
85 90 95

Leu Gly Ala Asp Asp Leu Thr Pro Phe Gly Glu Gln Gln Met Val Asn
100 105 110

Ser Gly Ile Lys Phe Tyr Arg Arg Tyr Lys Ala Leu Ala Arg Lys Ile
115 120 125

Val Pro Phe Val Arg Ala Ser Gly Ser Asp Arg Val Ile Ala Ser Ala
130 135 140

Glu Lys Phe Ile Glu Gly Phe Gln Ser Ala Lys Leu Ala Asp Pro Gly
145 150 155 160

Ala Asn Pro His Gln Ala Ser Pro Val Ile Asn Val Ile Ile Pro Glu
165 170 175

Gly Ala Gly Tyr Asn Asn Thr Leu Asp His Gly Leu Cys Thr Ala Phe
180 185 190

Glu Glu Ser Glu Leu Gly Asp Asp Val Glu Ala Asn Phe Thr Ala Val
195 200 205

Phe Ala Pro Pro Ile Arg Ala Arg Leu Glu Ala His Leu Pro Gly Val
210 215 220

Asn Leu Thr Asp Glu Asp Val Val Asn Leu Met Asp Met Cys Pro Phe
225 230 235 240

Asp Thr Val Ala Arg Thr Ser Asp Ala Thr Gln Leu Ser Pro Phe Cys
245 250 255

Asp Leu Phe Thr His Asp Glu Trp Ile Gln Tyr Asp Tyr Leu Gln Ser
260 265 270

Leu Gly Lys Tyr Tyr Gly Tyr Gly Ala Gly Asn Pro Leu Gly Pro Ala
275 280 285

Gln Gly Val Gly Phe Val Asn Glu Leu Ile Ala Arg Leu Thr His Ser
290 295 300

Pro Val Gln Asp His Thr Ser Thr Asn His Thr Leu Asp Ser Asn Pro
305 310 315 320

Ala Thr Phe Pro Leu Asn Ala Thr Leu Tyr Ala Asp Phe Ser His Asp
325 330 335

Asn Thr Met Val Ser Ile Phe Phe Ala Leu Gly Leu Tyr Asn Gly Thr
340 345 350

Lys Pro Leu Ser Thr Thr Ser Val Glu Ser Ile Glu Glu Thr Asp Gly
355 360 365

Tyr Ala Ala Ser Trp Thr Val Pro Phe Ala Ala Arg Ala Tyr Val Glu
370 375 380

Met Met Gln Cys Glu Ala Glu Lys Glu Pro Leu Val Arg Val Leu Val
385 390 395 400

Asn Asp Arg Val Val Pro Leu His Gly Cys Gly Val Asp Lys Leu Gly
405 410 415

Arg Cys Lys Arg Asp Asp Phe Val Glu Gly Leu Ser Phe Ala Arg Ser
420 425 430

Gly Gly Asn Trp Glu Glu Cys Phe Ala
435 440

<210> 25
<211> 1426
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<220>
<221> CDS
<222> (12)..(1412)
<223>

<220>
<221> mat_peptide
<222> (90)..()

<223>

<220>

<221> sig_peptide
<222> (12) .. (89)
<223>

<400> 25

tatataatt c atg ggc gtg ttc gtc gtg cta ctg tcc att gcc acc ttg 50
Met Gly Val Phe Val Val Leu Leu Ser Ile Ala Thr Leu
-25 -20 -15

ttc ggt tcc aca tcc ggt acc gcc ttg ggt cct cgt ggt aat tct cac 98
Phe Gly Ser Thr Ser Gly Thr Ala Leu Gly Pro Arg Gly Asn Ser His
-10 -5 -1 1

tct tgt gac act gtt gac ggt tac caa tgt ttc cca gaa att tct 146
Ser Cys Asp Thr Val Asp Gly Gly Tyr Gln Cys Phe Pro Glu Ile Ser
5 10 15

cac ttg tgg ggt caa tac tct cca ttc ttc tct ttg gct gac gaa tct 194
His Leu Trp Gly Gln Tyr Ser Pro Phe Phe Ser Leu Ala Asp Glu Ser
20 25 30 35

gct att tct cca gac gtt cca aag ggt tgt aga gtt act ttc gtt caa 242
Ala Ile Ser Pro Asp Val Pro Lys Gly Cys Arg Val Thr Phe Val Gln
40 45 50

gtt ttg tct aga cac ggt gct aga tac cca act tct tct aag tct aag 290
Val Leu Ser Arg His Gly Ala Arg Tyr Pro Thr Ser Ser Lys Ser Lys
55 60 65

aag tac tct gct ttg att gaa gct att caa aag aac gct act gct ttc 338
Lys Tyr Ser Ala Leu Ile Glu Ala Ile Gln Lys Asn Ala Thr Ala Phe
70 75 80

aag ggt aag tac gct ttc ttg aag act tac aac tac act ttg ggt gct 386
Lys Gly Lys Tyr Ala Phe Leu Lys Thr Tyr Asn Tyr Thr Leu Gly Ala
85 90 95

gac gac ttg act cca ttc ggt gaa caa caa atg gtt aac tct ggt att 434
Asp Asp Leu Thr Pro Phe Gly Glu Gln Gln Met Val Asn Ser Gly Ile
100 105 110 115

aag ttc tac aga aga tac aag gct ttg gct aga aag att gtt cca ttc 482
Lys Phe Tyr Arg Arg Tyr Lys Ala Leu Ala Arg Lys Ile Val Pro Phe
120 125 130

gtt aga gct tct ggt tct gac aga gtt att gct tct gct gaa aag ttc 530
Val Arg Ala Ser Gly Ser Asp Arg Val Ile Ala Ser Ala Glu Lys Phe
135 140 145

att gaa ggt ttc caa tct gct aag ttg gct gac cca ggt gct aac cca 578
Ile Glu Gly Phe Gln Ser Ala Lys Leu Ala Asp Pro Gly Ala Asn Pro
150 155 160

cac caa gct tct cca gtt att aac gtt att att cca gaa ggt gct ggt 626

His Gln Ala Ser Pro Val Ile Asn Val Ile Ile Pro Glu Gly Ala Gly			
165	170	175	
tac aac aac act ttg gac cac ggt ttg tgt act gct ttc gaa gaa tct			674
Tyr Asn Asn Thr Leu Asp His Gly Leu Cys Thr Ala Phe Glu Glu Ser			
180	185	190	195
gaa ttg ggt gac gac gtt gaa gct aac ttc act gct gtt ttc gct cca			722
Glu Leu Gly Asp Asp Val Glu Ala Asn Phe Thr Ala Val Phe Ala Pro			
200	205	210	
cct att aga gct aga ttg gaa gct cac ttg cca ggt gtt aac ttg act			770
Pro Ile Arg Ala Arg Leu Glu Ala His Leu Pro Gly Val Asn Leu Thr			
215	220	225	
gac gaa gac gtt aac ttg atg gac atg tgt cca ttc gac act gtt			818
Asp Glu Asp Val Val Asn Leu Met Asp Met Cys Pro Phe Asp Thr Val			
230	235	240	
gct aga act tct gac gct act caa ttg tct cca ttc tgt gac ttg ttc			866
Ala Arg Thr Ser Asp Ala Thr Gln Leu Ser Pro Phe Cys Asp Leu Phe			
245	250	255	
act cac gac gaa tgg att caa tac gac tac ttg caa tct ttg ggt aag			914
Thr His Asp Glu Trp Ile Gln Tyr Asp Tyr Leu Gln Ser Leu Gly Lys			
260	265	270	275
tac tac ggt tac ggt gct aac cca ttg ggt cca gct caa ggt gtt			962
Tyr Tyr Gly Tyr Gly Ala Gly Asn Pro Leu Gly Pro Ala Gln Gly Val			
280	285	290	
ggt ttc gtt aac gaa ttg att gct aga ttg act cac tct cca gtt caa			1010
Gly Phe Val Asn Glu Leu Ile Ala Arg Leu Thr His Ser Pro Val Gln			
295	300	305	
gac cac act tct act aac cac act ttg gac tct aac cca gct act ttc			1058
Asp His Thr Ser Thr Asn His Thr Leu Asp Ser Asn Pro Ala Thr Phe			
310	315	320	
cca ttg aac gct act ttg tac gct gac ttc tct cac gac aac act atg			1106
Pro Leu Asn Ala Thr Leu Tyr Ala Asp Phe Ser His Asp Asn Thr Met			
325	330	335	
gtt tct att ttc ttc gct ttg ggt ttg tac aac ggt act aag cca ttg			1154
Val Ser Ile Phe Phe Ala Leu Gly Leu Tyr Asn Gly Thr Lys Pro Leu			
340	345	350	355
tct act act tct gtt gaa tct att gaa gaa act gac ggt tac gct gct			1202
Ser Thr Thr Ser Val Glu Ser Ile Glu Glu Thr Asp Gly Tyr Ala Ala			
360	365	370	
tct tgg act gtt cca ttc gct gct aga gct tac gtt gaa atg atg caa			1250
Ser Trp Thr Val Pro Phe Ala Ala Arg Ala Tyr Val Glu Met Met Gln			
375	380	385	
tgt gaa gct gaa aag gaa cca ttg gtt aga gtt ttg gtt aac gac aga			1298
Cys Glu Ala Glu Lys Glu Pro Leu Val Arg Val Leu Val Asn Asp Arg			

390

395

400

gtt gtt cca ttg cac ggt tgt ggt gtt gac aag ttg ggt aga tgt aag 1346
Val Val Pro Leu His Gly Cys Gly Val Asp Lys Leu Gly Arg Cys Lys
405 410 415

aga gac gac ttc gtt gaa ggt ttg tct ttc gct aga tct ggt aac 1394
Arg Asp Asp Phe Val Glu Gly Leu Ser Phe Ala Arg Ser Gly Gly Asn
420 425 430 435

tgg gaa gaa tgt ttc gct taagaattca tata 1426
Trp Glu Glu Cys Phe Ala
440

<210> 26
<211> 467
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 26

Met Gly Val Phe Val Val Leu Leu Ser Ile Ala Thr Leu Phe Gly Ser
-25 -20 -15

Thr Ser Gly Thr Ala Leu Gly Pro Arg Gly Asn Ser His Ser Cys Asp
-10 -5 -1 1 5

Thr Val Asp Gly Gly Tyr Gln Cys Phe Pro Glu Ile Ser His Leu Trp
10 15 20

Gly Gln Tyr Ser Pro Phe Phe Ser Leu Ala Asp Glu Ser Ala Ile Ser
25 30 35

Pro Asp Val Pro Lys Gly Cys Arg Val Thr Phe Val Gln Val Leu Ser
40 45 50

Arg His Gly Ala Arg Tyr Pro Thr Ser Ser Lys Ser Lys Lys Tyr Ser
55 60 65 70

Ala Leu Ile Glu Ala Ile Gln Lys Asn Ala Thr Ala Phe Lys Gly Lys
75 80 85

Tyr Ala Phe Leu Lys Thr Tyr Asn Tyr Thr Leu Gly Ala Asp Asp Leu
90 95 100

Thr Pro Phe Gly Glu Gln Gln Met Val Asn Ser Gly Ile Lys Phe Tyr
105 110 115

Arg Arg Tyr Lys Ala Leu Ala Arg Lys Ile Val Pro Phe Val Arg Ala
120 125 130

Ser Gly Ser Asp Arg Val Ile Ala Ser Ala Glu Lys Phe Ile Glu Gly
135 140 145 150

Phe Gln Ser Ala Lys Leu Ala Asp Pro Gly Ala Asn Pro His Gln Ala
155 160 165

Ser Pro Val Ile Asn Val Ile Ile Pro Glu Gly Ala Gly Tyr Asn Asn
170 175 180

Thr Leu Asp His Gly Leu Cys Thr Ala Phe Glu Glu Ser Glu Leu Gly
185 190 195

Asp Asp Val Glu Ala Asn Phe Thr Ala Val Phe Ala Pro Pro Ile Arg
200 205 210

Ala Arg Leu Glu Ala His Leu Pro Gly Val Asn Leu Thr Asp Glu Asp
215 220 225 230

Val Val Asn Leu Met Asp Met Cys Pro Phe Asp Thr Val Ala Arg Thr
235 240 245

Ser Asp Ala Thr Gln Leu Ser Pro Phe Cys Asp Leu Phe Thr His Asp
250 255 260

Glu Trp Ile Gln Tyr Asp Tyr Leu Gln Ser Leu Gly Lys Tyr Tyr Gly
265 270 275

Tyr Gly Ala Gly Asn Pro Leu Gly Pro Ala Gln Gly Val Gly Phe Val
280 285 290

Asn Glu Leu Ile Ala Arg Leu Thr His Ser Pro Val Gln Asp His Thr
295 300 305 310

Ser Thr Asn His Thr Leu Asp Ser Asn Pro Ala Thr Phe Pro Leu Asn
315 320 325

Ala Thr Leu Tyr Ala Asp Phe Ser His Asp Asn Thr Met Val Ser Ile

330

335

340

Phe Phe Ala Leu Gly Leu Tyr Asn Gly Thr Lys Pro Leu Ser Thr Thr
345 350 355

Ser Val Glu Ser Ile Glu Glu Thr Asp Gly Tyr Ala Ala Ser Trp Thr
360 365 370

Val Pro Phe Ala Ala Arg Ala Tyr Val Glu Met Met Gln Cys Glu Ala
375 380 385 390

Glu Lys Glu Pro Leu Val Arg Val Leu Val Asn Asp Arg Val Val Pro
395 400 405

Leu His Gly Cys Gly Val Asp Lys Leu Gly Arg Cys Lys Arg Asp Asp
410 415 420

Phe Val Glu Gly Leu Ser Phe Ala Arg Ser Gly Gly Asn Trp Glu Glu
425 430 435

Cys Phe Ala
440

<210> 27
<211> 437
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 27

Asn Ser His Ser Cys Asp Thr Val Asp Gly Tyr Gln Cys Pro Glu Ile
1 5 10 15

Ser His Leu Trp Gly Gln Tyr Ser Pro Phe Phe Ser Leu Ala Asp Glu
20 25 30

Ser Ala Ile Ser Pro Asp Val Pro Lys Gly Cys Arg Val Thr Phe Val
35 40 45

Gln Val Leu Ser Arg His Gly Ala Arg Tyr Pro Thr Ser Ser Lys Ser
50 55 60

Lys Lys Tyr Ser Ala Leu Ile Glu Arg Ile Gln Lys Asn Ala Thr Phe
65 70 75 80

Lys Gly Lys Tyr Ala Phe Leu Lys Thr Tyr Asn Tyr Thr Leu Gly Ala
85 90 95

Asp Asp Leu Thr Pro Phe Gly Glu Asn Gln Met Val Asn Ser Gly Ile
100 105 110

Lys Phe Tyr Arg Arg Tyr Lys Ala Leu Ala Arg Asn Ile Val Pro Phe
115 120 125

Val Arg Ala Ser Gly Ser Asp Arg Val Ile Ala Ser Ala Glu Lys Phe
130 135 140

Ile Glu Gly Phe Gln Ser Ala Lys Leu Ala Asp Pro Ala His Gln Ala
145 150 155 160

Ser Pro Val Ile Asn Val Ile Ile Pro Glu Gly Ser Gly Tyr Asn Asn
165 170 175

Thr Leu Asp His Gly Leu Cys Thr Ala Phe Glu Asp Ser Thr Leu Gly
180 185 190

Asp Asp Ala Glu Ala Asn Phe Thr Ala Val Phe Ala Pro Pro Ile Arg
195 200 205

Ala Arg Leu Glu Ala Leu Pro Gly Val Asn Leu Thr Asp Glu Asp Val
210 215 220

Val Asn Leu Met Asp Met Cys Pro Phe Asp Thr Val Ala Arg Thr Ser
225 230 235 240

Asp Ala Thr Gln Leu Ser Pro Phe Cys Asp Leu Phe Thr Ala Asp Glu
245 250 255

Trp Gln Tyr Asp Tyr Leu Gln Ser Leu Lys Tyr Tyr Gly Tyr Gly Ala
260 265 270

Gly Asn Pro Leu Gly Pro Ala Gln Gly Val Gly Phe Asn Glu Leu Ile
275 280 285

Ala Arg Leu Thr His Ser Pro Val Gln Asp His Thr Ser Thr Asn His

290

295

300

Thr Leu Asp Ser Asn Pro Ala Thr Phe Pro Leu Asn Ala Thr Leu Tyr
 305 310 315 320

Ala Asp Phe Ser His Asp Asn Thr Met Val Ser Ile Phe Phe Ala Leu
325 330 335

Gly Leu Tyr Asn Gly Thr Lys Pro Leu Ser Thr Thr Ser Val Glu Ser
340 345 350

Ile Glu Thr Asp Gly Tyr Ala Ala Ser Trp Thr Val Pro Phe Ala Ala
355 360 365

Arg Ala Tyr Val Glu Met Met Gln Cys Glu Ala Gly Gly Gly Gly Gly
370 375 380

Glu Gly Glu Lys Glu Pro Leu Val Arg Val Leu Val Asn Asp Arg Val
 385 390 395 400

Val Pro Leu His Gly Cys Gly Val Asp Lys Leu Gly Arg Cys Lys Leu
 405 410 415

Asp Asp Phe Val Glu Gly Leu Ser Phe Ala Arg Ser Gly Gly Asn Trp
420 425 430

Ala Glu Cys Phe Ala
435

<210> 28
<211> 1404
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<220>
<221> CDS
<222> (1) .. (1401)
<223>

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<220>
<221> mat_peptide
<222> (79)..()
<223>
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<220>
<221> sig_peptide
<222> (1)..(78)
<223>

<400> 28
atg ggc gtg ttc gtc gtg cta ctg tcc att gcc acc ttg ttc ggt tcc      48
Met Gly Val Phe Val Val Leu Leu Ser Ile Ala Thr Leu Phe Gly Ser
-25          -20          -15

aca tcc ggt acc gcc ttg ggt cct cgt ggt aat tct cac tct tgt gac      96
Thr Ser Gly Thr Ala Leu Gly Pro Arg Gly Asn Ser His Ser Cys Asp
-10          -5           -1   1           5

act gtt gac ggt ggt tac caa tgt ttc cca gaa att tct cac ttg tgg      144
Thr Val Asp Gly Gly Tyr Gln Cys Phe Pro Glu Ile Ser His Leu Trp
10           15           20

ggt acc tac tct cca tac ttc tct ttg gca gac gaa tct gct att tct      192
Gly Thr Tyr Ser Pro Tyr Phe Ser Leu Ala Asp Glu Ser Ala Ile Ser
25           30           35

cca gac gtt cca gac gac tgt aga gtt act ttc gtt caa gtt ttg tct      240
Pro Asp Val Pro Asp Asp Cys Arg Val Thr Phe Val Gln Val Leu Ser
40           45           50

aga cac ggt aga tac cca act tct tct gcg tct aag gct tac tct      288
Arg His Gly Ala Arg Tyr Pro Thr Ser Ser Ala Ser Lys Ala Tyr Ser
55           60           65           70

gct ttg att gaa gct att caa aag aac gct act gct ttc aag ggt aag      336
Ala Leu Ile Glu Ala Ile Gln Lys Asn Ala Thr Ala Phe Lys Gly Lys
75           80           85

tac gct ttc ttg aag act tac aac tac act ttg ggt gct gac gac ttg      384
Tyr Ala Phe Leu Lys Thr Tyr Asn Tyr Thr Leu Gly Ala Asp Asp Leu
90           95          100

act cca ttc ggt gaa aac caa atg gtt aac tct ggt att aag ttc tac      432
Thr Pro Phe Gly Glu Asn Gln Met Val Asn Ser Gly Ile Lys Phe Tyr
105          110          115

aga aga tac aag gct ttg gct aga aag att gtt cca ttc att aga gct      480
Arg Arg Tyr Lys Ala Leu Ala Arg Lys Ile Val Pro Phe Ile Arg Ala
120          125          130

tct ggt tct gac aga gtt att gct tct gct gaa aag ttc att gaa ggt      528
Ser Gly Ser Asp Arg Val Ile Ala Ser Ala Glu Lys Phe Ile Glu Gly
135          140          145          150

ttc caa tct gct aag ttg gct gac cca ggt tct caa cca cac caa gct      576
Phe Gln Ser Ala Lys Leu Ala Asp Pro Gly Ser Gln Pro His Gln Ala
155          160          165

tct cca gtt att aac gtg atc att cca gaa gga tcc ggt tac aac aac      624
Ser Pro Val Ile Asn Val Ile Ile Pro Glu Gly Ser Gly Tyr Asn Asn
170          175          180

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act ttg gac cac ggt act tgt act gct ttc gaa gac tct gaa tta ggt		672
Thr Leu Asp His Gly Thr Cys Thr Ala Phe Glu Asp Ser Glu Leu Gly		
185	190	195
gac gac gtt gaa gct aac ttc act gct ttg ttc gct cca gct att aga		720
Asp Asp Val Glu Ala Asn Phe Thr Ala Leu Phe Ala Pro Ala Ile Arg		
200	205	210
gct aga ttg gaa gct gac ttg cca ggt gtt act ttg act gac gaa gac		768
Ala Arg Leu Glu Ala Asp Leu Pro Gly Val Thr Leu Thr Asp Glu Asp		
215	220	225
230		
gtt gtt tac ttg atg gac atg tgt cca ttc gac act gtc gct aga act		816
Val Val Tyr Leu Met Asp Met Cys Pro Phe Asp Thr Val Ala Arg Thr		
235	240	245
tct gac gct act gaa ttg tct cca ttc tgt gct ttg ttc act cac gac		864
Ser Asp Ala Thr Glu Leu Ser Pro Phe Cys Ala Leu Phe Thr His Asp		
250	255	260
gaa tgg atc caa tac gac tac ttg caa agc ttg ggt aag tac tac ggt		912
Glu Trp Ile Gln Tyr Asp Tyr Leu Gln Ser Leu Gly Lys Tyr Tyr Gly		
265	270	275
tac ggt gct ggt aac cca ttg ggt cca gct caa ggt gtt ggt ttc gct		960
Tyr Gly Ala Gly Asn Pro Leu Gly Pro Ala Gln Gly Val Gly Phe Ala		
280	285	290
aac gaa ttg att gct aga ttg act cac tct cca gtt caa gac cac act		1008
Asn Glu Leu Ile Ala Arg Leu Thr His Ser Pro Val Gln Asp His Thr		
295	300	305
310		
tct act aac cac act ttg gac tct aac cca gct act ttc cca ttg aac		1056
Ser Thr Asn His Thr Leu Asp Ser Asn Pro Ala Thr Phe Pro Leu Asn		
315	320	325
gct act ttg tac gct gac ttc tct cac gac aac act atg ata tct att		1104
Ala Thr Leu Tyr Ala Asp Phe Ser His Asp Asn Thr Met Ile Ser Ile		
330	335	340
ttc ttc gct ttg ggt ttg tac aac ggt acc aag cca ttg tct act act		1152
Phe Phe Ala Leu Gly Leu Tyr Asn Gly Thr Lys Pro Leu Ser Thr Thr		
345	350	355
tct gtt gaa tct att gaa gaa act gac ggt tac tct gct tct tgg act		1200
Ser Val Glu Ser Ile Glu Glu Thr Asp Gly Tyr Ser Ala Ser Trp Thr		
360	365	370
gtt cca ttc gct gct aga gct tac gtt gaa atg atg caa tgt caa gct		1248
Val Pro Phe Ala Ala Arg Ala Tyr Val Glu Met Met Gln Cys Gln Ala		
375	380	385
390		
gaa aag gaa cca ttg gtt aga gtt ttg gtt aac gac aga gtt gtt cca		1296
Glu Lys Glu Pro Leu Val Arg Val Leu Val Asn Asp Arg Val Val Pro		
395	400	405

ttg cac ggt tgt gct gtc gac aag ttg ggt aga tgt aag aga gac gac 1344
Leu His Gly Cys Ala Val Asp Lys Leu Gly Arg Cys Lys Arg Asp Asp
410 415 420

ttc gtt gaa ggt ttg tct ttc gct aga tct ggt aac tgg gct gaa 1392
Phe Val Glu Gly Leu Ser Phe Ala Arg Ser Gly Gly Asn Trp Ala Glu
425 430 435

tgt ttc gct taa 1404
Cys Phe Ala
440

<210> 29
<211> 467
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 29

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Thr Ser Gly Thr Ala Leu Gly Pro Arg Gly Asn Ser His Ser Cys Asp
-10 -5 -1 1 5

Thr Val Asp Gly Gly Tyr Gln Cys Phe Pro Glu Ile Ser His Leu Trp
10 15 20

Gly Thr Tyr Ser Pro Tyr Phe Ser Leu Ala Asp Glu Ser Ala Ile Ser
25 30 35

Pro Asp Val Pro Asp Asp Cys Arg Val Thr Phe Val Gln Val Leu Ser
40 45 50

Arg His Gly Ala Arg Tyr Pro Thr Ser Ser Ala Ser Lys Ala Tyr Ser
55 60 65 70

Ala Leu Ile Glu Ala Ile Gln Lys Asn Ala Thr Ala Phe Lys Gly Lys
75 80 85

Tyr Ala Phe Leu Lys Thr Tyr Asn Tyr Thr Leu Gly Ala Asp Asp Leu
90 95 100

Thr Pro Phe Gly Glu Asn Gln Met Val Asn Ser Gly Ile Lys Phe Tyr
105 110 115

Arg Arg Tyr Lys Ala Leu Ala Arg Lys Ile Val Pro Phe Ile Arg Ala
120 125 130

Ser Gly Ser Asp Arg Val Ile Ala Ser Ala Glu Lys Phe Ile Glu Gly
135 140 145 150

Phe Gln Ser Ala Lys Leu Ala Asp Pro Gly Ser Gln Pro His Gln Ala
155 160 165

Ser Pro Val Ile Asn Val Ile Ile Pro Glu Gly Ser Gly Tyr Asn Asn
170 175 180

Thr Leu Asp His Gly Thr Cys Thr Ala Phe Glu Asp Ser Glu Leu Gly
185 190 195

Asp Asp Val Glu Ala Asn Phe Thr Ala Leu Phe Ala Pro Ala Ile Arg
200 205 210

Ala Arg Leu Glu Ala Asp Leu Pro Gly Val Thr Leu Thr Asp Glu Asp
215 220 225 230

Val Val Tyr Leu Met Asp Met Cys Pro Phe Asp Thr Val Ala Arg Thr
235 240 245

Ser Asp Ala Thr Glu Leu Ser Pro Phe Cys Ala Leu Phe Thr His Asp
250 255 260

Glu Trp Ile Gln Tyr Asp Tyr Leu Gln Ser Leu Gly Lys Tyr Tyr Gly
265 270 275

Tyr Gly Ala Gly Asn Pro Leu Gly Pro Ala Gln Gly Val Gly Phe Ala
280 285 290

Asn Glu Leu Ile Ala Arg Leu Thr His Ser Pro Val Gln Asp His Thr
295 300 305 310

Ser Thr Asn His Thr Leu Asp Ser Asn Pro Ala Thr Phe Pro Leu Asn
315 320 325

Ala Thr Leu Tyr Ala Asp Phe Ser His Asp Asn Thr Met Ile Ser Ile
330 335 340

Phe Phe Ala Leu Gly Leu Tyr Asn Gly Thr Lys Pro Leu Ser Thr Thr
 345 350 355

Ser Val Glu Ser Ile Glu Glu Thr Asp Gly Tyr Ser Ala Ser Trp Thr
360 365 370

Val	Pro	Phe	Ala	Ala	Arg	Ala	Tyr	Val	Glu	Met	Met	Gln	Cys	Gln	Ala
375					380					385					390

Glu Lys Glu Pro Leu Val Arg Val Leu Val Asn Asp Arg Val Val Pro
395 400 405

Leu His Gly Cys Ala Val Asp Lys Leu Gly Arg Cys Lys Arg Asp Asp
410 415 420

Phe Val Glu Gly Leu Ser Phe Ala Arg Ser Gly Gly Asn Trp Ala Glu
 425 430 435

Cys Phe Ala
440

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<212> DNA
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<223>

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<222> (1)..(78)
<223>
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Met Gly Val Phe Val Val Leu Leu Ser Ile Ala Thr Leu Phe Gly Ser
-25           -20           -15

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aca tcc ggt acc gcc ttg ggt cct cgt ggt aac tct cac tct tgt gac	96
Thr Ser Gly Thr Ala Leu Gly Pro Arg Gly Asn Ser His Ser Cys Asp	
-10 -5 -1 1 5	
act gtt gac ggt ggt tac caa tgt ttc cca gaa att tct cac ttg tgg	144
Thr Val Asp Gly Gly Tyr Gln Cys Phe Pro Glu Ile Ser His Leu Trp	
10 15 20	
ggt aca tac tct cca ttc ttc tct ttg gct gac gaa tct gct att tct	192
Gly Thr Tyr Ser Pro Phe Phe Ser Leu Ala Asp Glu Ser Ala Ile Ser	
25 30 35	
cca gac gtt cca aag ggt tgt aga gtt act ttc gtt caa gtt ttg tct	240
Pro Asp Val Pro Lys Gly Cys Arg Val Thr Phe Val Gln Val Leu Ser	
40 45 50	
aga cac ggt gct aga tac cca act tct tct gcg tct aag gcg tac tct	288
Arg His Gly Ala Arg Tyr Pro Thr Ser Ser Ala Ser Lys Ala Tyr Ser	
55 60 65 70	
gct ttg att gaa gct att caa aag aac gct act gct ttc aag ggt aag	336
Ala Leu Ile Glu Ala Ile Gln Lys Asn Ala Thr Ala Phe Lys Gly Lys	
75 80 85	
tac gct ttc ttg aag act tac aac tac act ttg ggt gct gac gac ttg	384
Tyr Ala Phe Leu Lys Thr Tyr Asn Tyr Thr Leu Gly Ala Asp Asp Leu	
90 95 100	
act cca ttc ggt gaa caa caa atg gtt aac tct ggt att aag ttc tac	432
Thr Pro Phe Gly Glu Gln Gln Met Val Asn Ser Gly Ile Lys Phe Tyr	
105 110 115	
aga aga tac aag gct ttg gct aga aag att gtt cca ttc att aga gct	480
Arg Arg Tyr Lys Ala Leu Ala Arg Lys Ile Val Pro Phe Ile Arg Ala	
120 125 130	
tct ggt tct gac aga gtt att gct tct gct gaa aag ttc att gaa ggt	528
Ser Gly Ser Asp Arg Val Ile Ala Ser Ala Glu Lys Phe Ile Glu Gly	
135 140 145 150	
ttc caa tct gct aag ttg gct gac cca ggt gct aac cca cac caa gct	576
Phe Gln Ser Ala Lys Leu Ala Asp Pro Gly Ala Asn Pro His Gln Ala	
155 160 165	
tct cca gtt att aac gtt att att cca gaa ggt gct ggt tac aac aac	624
Ser Pro Val Ile Asn Val Ile Ile Pro Glu Gly Ala Gly Tyr Asn Asn	
170 175 180	
act ttg gac cac ggt ttg tgt act gct ttc gaa gaa tct gaa ttg ggt	672
Thr Leu Asp His Gly Leu Cys Thr Ala Phe Glu Glu Ser Glu Leu Gly	
185 190 195	
gac gac gtt gaa gct aac ttc act gct gtt ttc gct cca cca att aga	720
Asp Asp Val Glu Ala Asn Phe Thr Ala Val Phe Ala Pro Pro Ile Arg	
200 205 210	
gct aga ttg gaa gct cac ttg cca ggt gtt aac ttg act gac gaa gac	768

Ala Arg Leu Glu Ala His Leu Pro Gly Val Asn Leu Thr Asp Glu Asp			
215	220	225	230
gtt gtt aac ttg atg gac atg tgt cca ttc gac act gtt gct aga act			816
Val Val Asn Leu Met Asp Met Cys Pro Phe Asp Thr Val Ala Arg Thr			
235	240	245	
tct gac gct act caa ttg tct cca ttc tgt gac ttg ttc act cac gac			864
Ser Asp Ala Thr Gln Leu Ser Pro Phe Cys Asp Leu Phe Thr His Asp			
250	255	260	
gaa tgg att caa tac gac tac ttg caa tct ttg ggt aag tac tac ggt			912
Glu Trp Ile Gln Tyr Asp Tyr Leu Gln Ser Leu Gly Lys Tyr Tyr Gly			
265	270	275	
tac ggt gct ggt aac cca ttg ggt cca gct caa ggt gtt ggt ttc gtt			960
Tyr Gly Ala Gly Asn Pro Leu Gly Pro Ala Gln Gly Val Gly Phe Val			
280	285	290	
aac gaa ttg att gct aga ttg act cac tct cca gtt caa gac cac act			1008
Asn Glu Leu Ile Ala Arg Leu Thr His Ser Pro Val Gln Asp His Thr			
295	300	305	310
tct act aac cac act ttg gac tct aac cca gct act ttc cca ttg aac			1056
Ser Thr Asn His Thr Leu Asp Ser Asn Pro Ala Thr Phe Pro Leu Asn			
315	320	325	
gct act ttg tac gct gac ttc tct cac gac aac act atg gtt tct att			1104
Ala Thr Leu Tyr Ala Asp Phe Ser His Asp Asn Thr Met Val Ser Ile			
330	335	340	
ttc ttc gct ttg ggt ttg tac aac ggt act aag cca ttg tct act act			1152
Phe Phe Ala Leu Gly Leu Tyr Asn Gly Thr Lys Pro Leu Ser Thr Thr			
345	350	355	
tct gtt gaa tct att gaa gaa act gac ggt tac tct gct tct tgg act			1200
Ser Val Glu Ser Ile Glu Glu Thr Asp Gly Tyr Ser Ala Ser Trp Thr			
360	365	370	
gtt cca ttc gct gct aga gct tac gtt gaa atg atg caa tgt gaa gct			1248
Val Pro Phe Ala Ala Arg Ala Tyr Val Glu Met Met Gln Cys Glu Ala			
375	380	385	390
gaa aag gaa cca ttg gtt aga gtt ttg gtt aac gac aga gtt gtt cca			1296
Glu Lys Glu Pro Leu Val Arg Val Leu Val Asn Asp Arg Val Val Pro			
395	400	405	
ttg cac ggt tgt ggt gtt gac aag ttg ggt aga tgt aag aga gac gac			1344
Leu His Gly Cys Gly Val Asp Lys Leu Gly Arg Cys Lys Arg Asp Asp			
410	415	420	
ttc gtt gaa ggt ttg tct ttc gct aga tct ggt ggt aac tgg gaa gaa			1392
Phe Val Glu Gly Leu Ser Phe Ala Arg Ser Gly Gly Asn Trp Glu Glu			
425	430	435	
tgt ttc gct taa			1404
Cys Phe Ala			

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<400> 31

Met Gly Val Phe Val Val Leu Leu Ser Ile Ala Thr Leu Phe Gly Ser
-25 -20 -15

Thr Ser Gly Thr Ala Leu Gly Pro Arg Gly Asn Ser His Ser Cys Asp
-10 -5 -1 1 5

Thr Val Asp Gly Gly Tyr Gln Cys Phe Pro Glu Ile Ser His Leu Trp
10 15 20

Gly Thr Tyr Ser Pro Phe Phe Ser Leu Ala Asp Glu Ser Ala Ile Ser
25 30 35

Pro Asp Val Pro Lys Gly Cys Arg Val Thr Phe Val Gln Val Leu Ser
40 45 50

Arg His Gly Ala Arg Tyr Pro Thr Ser Ser Ala Ser Lys Ala Tyr Ser
55 60 65 70

Ala Leu Ile Glu Ala Ile Gln Lys Asn Ala Thr Ala Phe Lys Gly Lys
75 80 85

Tyr Ala Phe Leu Lys Thr Tyr Asn Tyr Thr Leu Gly Ala Asp Asp Leu
90 95 100

Thr Pro Phe Gly Glu Gln Gln Met Val Asn Ser Gly Ile Lys Phe Tyr
105 110 115

Arg Arg Tyr Lys Ala Leu Ala Arg Lys Ile Val Pro Phe Ile Arg Ala
120 125 130

Ser Gly Ser Asp Arg Val Ile Ala Ser Ala Glu Lys Phe Ile Glu Gly
135 140 145 150

Phe Gln Ser Ala Lys Leu Ala Asp Pro Gly Ala Asn Pro His Gln Ala
155 160 165

Ser Pro Val Ile Asn Val Ile Ile Pro Glu Gly Ala Gly Tyr Asn Asn
170 175 180

Thr Leu Asp His Gly Leu Cys Thr Ala Phe Glu Glu Ser Glu Leu Gly
185 190 195

Asp Asp Val Glu Ala Asn Phe Thr Ala Val Phe Ala Pro Pro Ile Arg
200 205 210

Ala Arg Leu Glu Ala His Leu Pro Gly Val Asn Leu Thr Asp Glu Asp
215 220 225 230

Val Val Asn Leu Met Asp Met Cys Pro Phe Asp Thr Val Ala Arg Thr
235 240 245

Ser Asp Ala Thr Gln Leu Ser Pro Phe Cys Asp Leu Phe Thr His Asp
250 255 260

Glu Trp Ile Gln Tyr Asp Tyr Leu Gln Ser Leu Gly Lys Tyr Tyr Gly
265 270 275

Tyr Gly Ala Gly Asn Pro Leu Gly Pro Ala Gln Gly Val Gly Phe Val
280 285 290

Asn Glu Leu Ile Ala Arg Leu Thr His Ser Pro Val Gln Asp His Thr
295 300 305 310

Ser Thr Asn His Thr Leu Asp Ser Asn Pro Ala Thr Phe Pro Leu Asn
315 320 325

Ala Thr Leu Tyr Ala Asp Phe Ser His Asp Asn Thr Met Val Ser Ile
330 335 340

Phe Phe Ala Leu Gly Leu Tyr Asn Gly Thr Lys Pro Leu Ser Thr Thr
345 350 355

Ser Val Glu Ser Ile Glu Glu Thr Asp Gly Tyr Ser Ala Ser Trp Thr
360 365 370

Val Pro Phe Ala Ala Arg Ala Tyr Val Glu Met Met Gln Cys Glu Ala

375	380	385	390
Glu Lys Glu Pro Leu Val Arg Val Leu Val Asn Asp Arg Val Val Pro			
395		400	405
Leu His Gly Cys Gly Val Asp Lys Leu Gly Arg Cys Lys Arg Asp Asp			
410	415		420
Phe Val Glu Gly Leu Ser Phe Ala Arg Ser Gly Gly Asn Trp Glu Glu			
425	430		435
Cys Phe Ala			
440			
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Met Gly Val Phe Val Val Leu Leu Ser Ile Ala Thr Leu Phe Gly Ser			
-25	-20		-15
48			
aca tcg ggc act gcg ctg ggc ccc cgt gga aat cac tcc aag tcc tgc			
Thr Ser Gly Thr Ala Leu Gly Pro Arg Gly Asn His Ser Lys Ser Cys			
-10	-5	-1	1
96			
-5			
5			
gat acg gta gac cta ggg tac cag tgc tcc cct gcg act tct cat cta			
Asp Thr Val Asp Leu Gly Tyr Gln Cys Ser Pro Ala Thr Ser His Leu			
10	15		20
144			
tgg ggc acg tac tcg cca tac ttt tcg ctc gag gac gag ctg tcc gtg			
Trp Gly Thr Tyr Ser Pro Tyr Phe Ser Leu Glu Asp Glu Leu Ser Val			
192			

25	30	35	
tcg agt aag ctt ccc aag gat tgc cg ^g atc acc ttg gta cag gtg cta Ser Ser Lys Leu Pro Lys Asp Cys Arg Ile Thr Leu Val Gln Val Leu	40	45	240
	50		
tcg cgc cat gga gc ^g cg ^g tac cca acc agc tcc aag agc aaa aag tat Ser Arg His Gly Ala Arg Tyr Pro Thr Ser Ser Lys Ser Lys Lys Tyr	55	60	288
		65	70
aag aag ctt att acg gc ^g atc cag gcc aat gcc acc gac ttc aag ggc Lys Lys Leu Ile Thr Ala Ile Gln Ala Asn Ala Thr Asp Phe Lys Gly	75	80	336
			85
aag tac gcc ttt ttg aag acg tac aac tat act ctg ggt gc ^g gat gac Lys Tyr Ala Phe Leu Lys Thr Tyr Asn Tyr Thr Leu Gly Ala Asp Asp	90	95	384
			100
ctc act ccc ttt ggg gag cag cag ctg gtg aac tcg ggc atc aag ttc Leu Thr Pro Phe Gly Glu Gln Gln Leu Val Asn Ser Gly Ile Lys Phe	105	110	432
			115
tac cag agg tac aag gct ctg gc ^g cgc agt gtg gtg ccg ttt att cgc Tyr Gln Arg Tyr Lys Ala Leu Ala Arg Ser Val Val Pro Phe Ile Arg	120	125	480
			130
gcc tca ggc tcg gac cg ^g gtt att gct tcg gga gag aag ttc atc gag Ala Ser Gly Ser Asp Arg Val Ile Ala Ser Gly Glu Lys Phe Ile Glu	135	140	528
			145
			150
ggg ttc cag cag gc ^g aag ctg gct gat cct ggc gc ^g acg aac cgc gcc Gly Phe Gln Gln Ala Lys Leu Ala Asp Pro Gly Ala Thr Asn Arg Ala	155	160	576
			165
gct ccg gc ^g att agt gtg att att ccg gag agc gag acg ttc aac aat Ala Pro Ala Ile Ser Val Ile Ile Pro Glu Ser Glu Thr Phe Asn Asn	170	175	624
			180
acg ctg gac cac ggt gtg tgc acg aag ttt gag gc ^g agt cag ctg gga Thr Leu Asp His Gly Val Cys Thr Lys Phe Glu Ala Ser Gln Leu Gly	185	190	672
			195
gat gag gtt gc ^g gcc aat ttc act gc ^g ctc ttt gca ccc gac atc cga Asp Glu Val Ala Ala Asn Phe Thr Ala Leu Phe Ala Pro Asp Ile Arg	200	205	720
			210
gct cgc ctc gag aag cat ctt cct gc ^g gtg acg ctg aca gac gag gac Ala Arg Leu Glu Lys His Leu Pro Gly Val Thr Leu Thr Asp Glu Asp	215	220	768
			225
			230
gtt gtc agt cta atg gac atg tgt ccg ttt gat acg gta gc ^g cgc acc Val Val Ser Leu Met Asp Met Cys Pro Phe Asp Thr Val Ala Arg Thr	235	240	816
			245
agc gac gca agt cag ctg tca ccg ttc tgt caa ctc ttc act cac aat Ser Asp Ala Ser Gln Leu Ser Pro Phe Cys Gln Leu Phe Thr His Asn	250	255	864
			260

gag tgg aag aag tac gac tac ctt cag tcc ttg ggc aag tac tac ggc Glu Trp Lys Lys Tyr Asp Tyr Leu Gln Ser Leu Gly Lys Tyr Tyr Gly	265	270	275	912
tac ggc gca ggc aac cct ctg gga ccg gct cag ggg ata ggg ttc acc Tyr Gly Ala Gly Asn Pro Leu Gly Pro Ala Gln Gly Ile Gly Phe Thr	280	285	290	960
aac gag ctg att gcc cggttg acg cgt tcg cca gtg cag gac cac acc Asn Glu Leu Ile Ala Arg Leu Thr Arg Ser Pro Val Gln Asp His Thr	295	300	305	1008
agc act aac tcg act cta gtc tcc aac ccg gcc acc ttc ccg ttg aac Ser Thr Asn Ser Thr Leu Val Ser Asn Pro Ala Thr Phe Pro Leu Asn	315	320	325	1056
gct acc atg tac gtc gac ttt tca cac gac aac agc atg gtt tcc atc Ala Thr Met Tyr Val Asp Phe Ser His Asp Asn Ser Met Val Ser Ile	330	335	340	1104
ttc ttt gca ttg ggc ctg tac aac ggc act gaa ccc ttg tcc ccg acc Phe Phe Ala Leu Gly Leu Tyr Asn Gly Thr Glu Pro Leu Ser Arg Thr	345	350	355	1152
tcg gtg gaa agc gcc aag gaa ttg gat ggg tat tct gca tcc tgg gtg Ser Val Glu Ser Ala Lys Glu Leu Asp Gly Tyr Ser Ala Ser Trp Val	360	365	370	1200
gtg cct ttc ggc gcg cga gcc tac ttc gag acg atg caa tgc aag tcg Val Pro Phe Gly Ala Arg Ala Tyr Phe Glu Thr Met Gln Cys Lys Ser	375	380	385	1248
gaa aag gag cct ctt gtt cgc qct ttg att aat gac ccg gtt gtg cca Glu Lys Glu Pro Leu Val Arg Ala Leu Ile Asn Asp Arg Val Val Pro	395	400	405	1296
ctg cat ggc tgc gat gtg gac aag ctg ggg cga tgc aag ctg aat gac Leu His Gly Cys Asp Val Asp Lys Leu Gly Arg Cys Lys Leu Asn Asp	410	415	420	1344
ttt gtc aag gga ttg agt tgg gcc aga tct ggg ggc aac tgg gga gag Phe Val Lys Gly Leu Ser Trp Ala Arg Ser Gly Gly Asn Trp Gly Glu	425	430	435	1392
tgc ttt agt tga Cys Phe Ser				1404
	440			

<210> 33
<211> 467
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 33

Met Gly Val Phe Val Val Leu Leu Ser Ile Ala Thr Leu Phe Gly Ser
-25 -20 -15

Thr Ser Gly Thr Ala Leu Gly Pro Arg Gly Asn His Ser Lys Ser Cys
-10 -5 -1 1 5

Asp Thr Val Asp Leu Gly Tyr Gln Cys Ser Pro Ala Thr Ser His Leu
10 15 20

Trp Gly Thr Tyr Ser Pro Tyr Phe Ser Leu Glu Asp Glu Leu Ser Val
25 30 35

Ser Ser Lys Leu Pro Lys Asp Cys Arg Ile Thr Leu Val Gln Val Leu
40 45 50

Ser Arg His Gly Ala Arg Tyr Pro Thr Ser Ser Lys Ser Lys Lys Tyr
55 60 65 70

Lys Lys Leu Ile Thr Ala Ile Gln Ala Asn Ala Thr Asp Phe Lys Gly
75 80 85

Lys Tyr Ala Phe Leu Lys Thr Tyr Asn Tyr Thr Leu Gly Ala Asp Asp
90 95 100

Leu Thr Pro Phe Gly Glu Gln Gln Leu Val Asn Ser Gly Ile Lys Phe
105 110 115

Tyr Gln Arg Tyr Lys Ala Leu Ala Arg Ser Val Val Pro Phe Ile Arg
120 125 130

Ala Ser Gly Ser Asp Arg Val Ile Ala Ser Gly Glu Lys Phe Ile Glu
135 140 145 150

Gly Phe Gln Gln Ala Lys Leu Ala Asp Pro Gly Ala Thr Asn Arg Ala
155 160 165

Ala Pro Ala Ile Ser Val Ile Ile Pro Glu Ser Glu Thr Phe Asn Asn
170 175 180

Thr Leu Asp His Gly Val Cys Thr Lys Phe Glu Ala Ser Gln Leu Gly
185 190 195

Asp Glu Val Ala Ala Asn Phe Thr Ala Leu Phe Ala Pro Asp Ile Arg
200 205 210

Ala Arg Leu Glu Lys His Leu Pro Gly Val Thr Leu Thr Asp Glu Asp
215 220 225 230

Val Val Ser Leu Met Asp Met Cys Pro Phe Asp Thr Val Ala Arg Thr
235 240 245

Ser Asp Ala Ser Gln Leu Ser Pro Phe Cys Gln Leu Phe Thr His Asn
250 255 260

Glu Trp Lys Lys Tyr Asp Tyr Leu Gln Ser Leu Gly Lys Tyr Tyr Gly
265 270 275

Tyr Gly Ala Gly Asn Pro Leu Gly Pro Ala Gln Gly Ile Gly Phe Thr
280 285 290

Asn Glu Leu Ile Ala Arg Leu Thr Arg Ser Pro Val Gln Asp His Thr
295 300 305 310

Ser Thr Asn Ser Thr Leu Val Ser Asn Pro Ala Thr Phe Pro Leu Asn
315 320 325

Ala Thr Met Tyr Val Asp Phe Ser His Asp Asn Ser Met Val Ser Ile
330 335 340

Phe Phe Ala Leu Gly Leu Tyr Asn Gly Thr Glu Pro Leu Ser Arg Thr
345 350 355

Ser Val Glu Ser Ala Lys Glu Leu Asp Gly Tyr Ser Ala Ser Trp Val
360 365 370

Val Pro Phe Gly Ala Arg Ala Tyr Phe Glu Thr Met Gln Cys Lys Ser
375 380 385 390

Glu Lys Glu Pro Leu Val Arg Ala Leu Ile Asn Asp Arg Val Val Pro
395 400 405

Leu His Gly Cys Asp Val Asp Lys Leu Gly Arg Cys Lys Leu Asn Asp
410 415 420

Phe Val Lys Gly Leu Ser Trp Ala Arg Ser Gly Gly Asn Trp Gly Glu
425 430 435

Cys Phe Ser
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Met Gly Val Phe Val Val Leu Leu Ser Ile Ala Thr Leu
-25 -20 -15

ttc ggt tcc aca tcc ggt acc gcc ttg ggt cct cgt ggt aat tct cac 98
Phe Gly Ser Thr Ser Gly Thr Ala Leu Gly Pro Arg Gly Asn Ser His
-10 -5 -1 1

tct tgt gac act gtt gac ggt ggt tac caa tgt ttc cca gaa att tct 146
Ser Cys Asp Thr Val Asp Gly Gly Tyr Gln Cys Phe Pro Glu Ile Ser
5 10 15

cac ttg tgg ggt caa tac tct cca tac ttc tct ttg gaa gac gaa tct 194
His Leu Trp Gly Gln Tyr Ser Pro Tyr Phe Ser Leu Glu Asp Glu Ser
20 25 30 35

gct att tct cca gac gtt cca gac gac tgt aga gtt act ttc gtt caa 242
Ala Ile Ser Pro Asp Val Pro Asp Asp Cys Arg Val Thr Phe Val Gln
40 45 50

gtt ttg tct aga cac ggt gct aga tac cca act gac tct aag ggt aag 290
Val Leu Ser Arg His Gly Ala Arg Tyr Pro Thr Asp Ser Lys Gly Lys
55 60 65

aag tac tct gct ttg att gaa gct att caa aag aac gct act gct ttc Lys Tyr Ser Ala Leu Ile Glu Ala Ile Gln Lys Asn Ala Thr Ala Phe 70 75 80	338
aag ggt aag tac gct ttc ttg aag act tac aac tac act ttg ggt gct Lys Gly Lys Tyr Ala Phe Leu Lys Thr Tyr Asn Tyr Thr Leu Gly Ala 85 90 95	386
gac gac ttg act cca ttc ggt gaa aac caa atg gtt aac tct ggt att Asp Asp Leu Thr Pro Phe Gly Glu Asn Gln Met Val Asn Ser Gly Ile 100 105 110 115	434
aag ttc tac aga aga tac aag gct ttg gct aga aag att gtt cca ttc Lys Phe Tyr Arg Arg Tyr Lys Ala Leu Ala Arg Lys Ile Val Pro Phe 120 125 130	482
att aga gct tct ggt tct aga gtt att gct tct gct gaa aag ttc Ile Arg Ala Ser Gly Ser Ser Arg Val Ile Ala Ser Ala Glu Lys Phe 135 140 145	530
att gaa ggt ttc caa tct gct aag ttg gct gac cca ggt tct caa cca Ile Glu Gly Phe Gln Ser Ala Lys Leu Ala Asp Pro Gly Ser Gln Pro 150 155 160	578
cac caa gct tct cca gtt att gac gtt att att tct gac gct tct tct His Gln Ala Ser Pro Val Ile Asp Val Ile Ile Ser Asp Ala Ser Ser 165 170 175	626
tac aac aac act ttg gac cca ggt act tgt act gct ttc gaa gac tct Tyr Asn Asn Thr Leu Asp Pro Gly Thr Cys Thr Ala Phe Glu Asp Ser 180 185 190 195	674
gaa ttg gct gac act gtt gaa gct aac ttc act gct ttg ttc gct cca Glu Leu Ala Asp Thr Val Glu Ala Asn Phe Thr Ala Leu Phe Ala Pro 200 205 210	722
gct att aga gct aga ttg gaa gct gac ttg cca ggt gtt act ttg act Ala Ile Arg Ala Arg Leu Glu Ala Asp Leu Pro Gly Val Thr Leu Thr 215 220 225	770
gac act gaa gtt act tac ttg atg gac atg tgt tct ttc gaa act gtt Asp Thr Glu Val Thr Tyr Leu Met Asp Met Cys Ser Phe Glu Thr Val 230 235 240	818
gct aga act tct gac gct act gaa ttg tct cca ttc tgt gct ttg ttc Ala Arg Thr Ser Asp Ala Thr Glu Leu Ser Pro Phe Cys Ala Leu Phe 245 250 255	866
act cac gac gaa tgg aga cac tac gac tac ttg caa tct ttg aag aag Thr His Asp Glu Trp Arg His Tyr Asp Tyr Leu Gln Ser Leu Lys Lys 260 265 270 275	914
tac tac ggt cac ggt gct ggt aac cca ttg ggt cca act caa ggt gtt Tyr Tyr Gly His Gly Ala Gly Asn Pro Leu Gly Pro Thr Gln Gly Val 280 285 290	962
ggt ttc gct aac gaa ttg att gct aga ttg act aga tct cca gtt caa	1010

Gly Phe Ala Asn Glu Leu Ile Ala Arg Leu Thr Arg Ser Pro Val Gln			
295	300	305	
gac cac act tct act aac cac act ttg gac tct aac cca gct act ttc			1058
Asp His Thr Ser Thr Asn His Thr Leu Asp Ser Asn Pro Ala Thr Phe			
310	315	320	
cca ttg aac gct act ttg tac gct gac ttc tct cac gac aac ggt att			1106
Pro Leu Asn Ala Thr Leu Tyr Ala Asp Phe Ser His Asp Asn Gly Ile			
325	330	335	
att tct att ttc ttc gct ttg ggt ttg tac aac ggt act gct cca ttg			1154
Ile Ser Ile Phe Phe Ala Leu Gly Leu Tyr Asn Gly Thr Ala Pro Leu			
340	345	350	355
tct act act tct gtt gaa tct att gaa gaa act gac ggt tac tct tct			1202
Ser Thr Thr Ser Val Glu Ser Ile Glu Glu Thr Asp Gly Tyr Ser Ser			
360	365	370	
gct tgg act gtt cca ttc gct tct aga gct tac gtt gaa atg atg caa			1250
Ala Trp Thr Val Pro Phe Ala Ser Arg Ala Tyr Val Glu Met Met Gln			
375	380	385	
tgt caa gct gaa aag gaa cca ttg gtt aga gtt ttg gtt aac gac aga			1298
Cys Gln Ala Glu Lys Glu Pro Leu Val Arg Val Leu Val Asn Asp Arg			
390	395	400	
gtt gtt cca ttg cac ggt tgt gct gtt gac aag ttg ggt aga tgt aag			1346
Val Val Pro Leu His Gly Cys Ala Val Asp Lys Leu Gly Arg Cys Lys			
405	410	415	
aga gac gac ttc gtt gaa ggt ttg tct ttc gct aga tct ggt ggt aac			1394
Arg Asp Asp Phe Val Glu Gly Leu Ser Phe Ala Arg Ser Gly Gly Asn			
420	425	430	435
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Trp Ala Glu Cys Phe Ala			
440			

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<211> 467
<212> PRT
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<400> 35

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-25 -20 -15

Thr Ser Gly Thr Ala Leu Gly Pro Arg Gly Asn Ser His Ser Cys Asp
-10 -5 -1 1 5

Thr Val Asp Gly Gly Tyr Gln Cys Phe Pro Glu Ile Ser His Leu Trp
10 15 20

Gly Gln Tyr Ser Pro Tyr Phe Ser Leu Glu Asp Glu Ser Ala Ile Ser
25 30 35

Pro Asp Val Pro Asp Asp Cys Arg Val Thr Phe Val Gln Val Leu Ser
40 45 50

Arg His Gly Ala Arg Tyr Pro Thr Asp Ser Lys Gly Lys Lys Tyr Ser
55 60 65 70

Ala Leu Ile Glu Ala Ile Gln Lys Asn Ala Thr Ala Phe Lys Gly Lys
75 80 85

Tyr Ala Phe Leu Lys Thr Tyr Asn Tyr Thr Leu Gly Ala Asp Asp Leu
90 95 100

Thr Pro Phe Gly Glu Asn Gln Met Val Asn Ser Gly Ile Lys Phe Tyr
105 110 115

Arg Arg Tyr Lys Ala Leu Ala Arg Lys Ile Val Pro Phe Ile Arg Ala
120 125 130

Ser Gly Ser Ser Arg Val Ile Ala Ser Ala Glu Lys Phe Ile Glu Gly
135 140 145 150

Phe Gln Ser Ala Lys Leu Ala Asp Pro Gly Ser Gln Pro His Gln Ala
155 160 165

Ser Pro Val Ile Asp Val Ile Ile Ser Asp Ala Ser Ser Tyr Asn Asn
170 175 180

Thr Leu Asp Pro Gly Thr Cys Thr Ala Phe Glu Asp Ser Glu Leu Ala
185 190 195

Asp Thr Val Glu Ala Asn Phe Thr Ala Leu Phe Ala Pro Ala Ile Arg
200 205 210

Ala Arg Leu Glu Ala Asp Leu Pro Gly Val Thr Leu Thr Asp Thr Glu
215 220 225 230

Val Thr Tyr Leu Met Asp Met Cys Ser Phe Glu Thr Val Ala Arg Thr
235 240 245

Ser Asp Ala Thr Glu Leu Ser Pro Phe Cys Ala Leu Phe Thr His Asp
250 255 260

Glu Trp Arg His Tyr Asp Tyr Leu Gln Ser Leu Lys Lys Tyr Tyr Gly
265 270 275

His Gly Ala Gly Asn Pro Leu Gly Pro Thr Gln Gly Val Gly Phe Ala
280 285 290

Asn Glu Leu Ile Ala Arg Leu Thr Arg Ser Pro Val Gln Asp His Thr
295 300 305 310

Ser Thr Asn His Thr Leu Asp Ser Asn Pro Ala Thr Phe Pro Leu Asn
315 320 325

Ala Thr Leu Tyr Ala Asp Phe Ser His Asp Asn Gly Ile Ile Ser Ile
330 335 340

Phe Phe Ala Leu Gly Leu Tyr Asn Gly Thr Ala Pro Leu Ser Thr Thr
345 350 355

Ser Val Glu Ser Ile Glu Glu Thr Asp Gly Tyr Ser Ser Ala Trp Thr
360 365 370

Val Pro Phe Ala Ser Arg Ala Tyr Val Glu Met Met Gln Cys Gln Ala
375 380 385 390

Glu Lys Glu Pro Leu Val Arg Val Leu Val Asn Asp Arg Val Val Pro
395 400 405

Leu His Gly Cys Ala Val Asp Lys Leu Gly Arg Cys Lys Arg Asp Asp
410 415 420

Phe Val Glu Gly Leu Ser Phe Ala Arg Ser Gly Gly Asn Trp Ala Glu
425 430 435

Cys Phe Ala
440

<211> 467
<212> PRT
<213> Artificial Sequence

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<400> 36

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20 25 30

Thr Val Asp Gly Gly Tyr Gln Cys Phe Pro Glu Ile Ser Ser Asn Trp
35 40 45

Ser Pro Tyr Ser Pro Tyr Phe Ser Leu Ala Asp Glu Ser Ala Ile Ser
50 55 60

Pro Asp Val Pro Lys Gly Cys Arg Val Thr Phe Val Gln Val Leu Gln
65 70 75 80

Arg His Gly Ala Arg Phe Pro Thr Ser Gly Ala Ala Thr Arg Ile Ser
85 90 95

Ala Leu Ile Glu Ala Ile Gln Lys Asn Ala Thr Ala Phe Lys Gly Lys
100 105 110

Tyr Ala Phe Leu Lys Thr Tyr Asn Tyr Thr Leu Gly Ala Asp Asp Leu
115 120 125

Val Pro Phe Gly Ala Asn Gln Ser Ser Gln Ala Gly Ile Lys Phe Tyr
130 135 140

Arg Arg Tyr Lys Ala Leu Ala Arg Lys Ile Val Pro Phe Ile Arg Ala
145 150 155 160

Ser Gly Ser Asp Arg Val Ile Asp Ser Ala Thr Asn Trp Ile Glu Gly
165 170 175

Phe Gln Ser Ala Lys Leu Ala Asp Pro Gly Ala Asn Pro His Gln Ala
180 185 190

Ser Pro Val Ile Asn Val Ile Ile Pro Glu Gly Ala Gly Tyr Asn Asn
195 200 205

Thr Leu Asp His Gly Leu Cys Thr Ala Phe Glu Glu Ser Glu Leu Gly
210 215 220

Asp Asp Val Glu Ala Asn Phe Thr Ala Val Phe Ala Pro Pro Ile Arg
225 230 235 240

Ala Arg Leu Glu Ala His Leu Pro Gly Val Asn Leu Thr Asp Glu Asp
245 250 255

Val Val Asn Leu Met Asp Met Cys Pro Phe Asp Thr Val Ala Arg Thr
260 265 270

Ser Asp Ala Thr Glu Leu Ser Pro Phe Cys Asp Leu Phe Thr His Asp
275 280 285

Glu Trp Ile Gln Tyr Asp Tyr Leu Gly Asp Leu Asp Lys Tyr Tyr Gly
290 295 300

Thr Gly Ala Gly Asn Pro Leu Gly Pro Ala Gln Gly Val Gly Phe Val
305 310 315 320

Asn Glu Leu Ile Ala Arg Leu Thr His Ser Pro Val Gln Asp His Thr
325 330 335

Ser Thr Asn His Thr Leu Asp Ser Asn Pro Ala Thr Phe Pro Leu Asn
340 345 350

Ala Thr Leu Tyr Ala Asp Phe Ser His Asp Asn Thr Met Val Ala Ile
355 360 365

Phe Phe Ala Leu Gly Leu Tyr Asn Gly Thr Lys Pro Leu Ser Thr Thr
370 375 380

Ser Val Glu Ser Ile Glu Glu Thr Asp Gly Tyr Ser Ala Ser Trp Leu
385 390 395 400

Val Pro Phe Ser Ala Arg Met Tyr Val Glu Met Met Gln Cys Glu Ala
405 410 415

Glu Lys Glu Pro Leu Val Arg Val Leu Val Asn Asp Arg Val Val Pro

420

425

430

Leu His Gly Cys Gly Val Asp Lys Leu Gly Arg Cys Lys Arg Asp Asp
435 440 445

Phe Val Glu Gly Leu Ser Phe Ala Arg Ser Gly Gly Asn Trp Glu Glu
450 455 460

Cys Phe Ala
465

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26

<210> 38
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<212> DNA
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<220>
<223> Primer

<400> 38
tggaaaagttc attgaaggtt tc

22

<210> 39
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<220>
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tccttcgaaag cagtacaccaa ac

22

<210> 40
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<400> 40
tatatgaatt cttaagcgaa ac 22

<210> 41
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ggtcaatact ctccattctt ctctttggaa g 31

<210> 43
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<400> 43
catacttctc tttggcagac gaatctgc 28

<210> 44
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ctccagacgt cccaaaggac ttagatgtta c 31

<210> 45
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<400> 45
ctccagacgt cccagacggc tgttagagtta c 31

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<400> 46
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cttctaagtc taagaagtac tctgctttg 29

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<400> 48
gcttaactctg ctttgattga acggattcaa aagaacgcta c 41

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ctccagttat taacgtgatc attccagaag g 31

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<400> 54

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32

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34

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<400> 56
ggtgacgacg ctgaagctaa cttcac

26

<210> 57
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<400> 57
ctaacttcac cgcggttgc gctccag

27

<210> 58
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<400> 64

gctttgttca ccgcggacga atggag

26

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<211> 27

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<400> 65

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27

<210> 66

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<400> 66

gacgaatgga gagcgtacga ctacttg

27

<210> 67

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<400> 67

ggtgttgggt tcgttaacga attgattgc

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<223> Primer

<400> 68

gctagattga ctcactctcc agttcaag

28

<210> 69

<211> 32

<212> DNA

<213> Artificial Sequence

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<210> 70

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<400> 70
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<210> 71

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<212> DNA

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<211> 25

<212> DNA

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<400> 72
ctgacggtta cgctgcttct tggac 25

<210> 73

<211> 26

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<213> Artificial Sequence

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<400> 73
ctgttccatt cgctgctaga gcttac 26

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<400> 74
gatcaatgt gaagctgaaa aggaacc 27

<210> 75
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<400> 75
cacggttgtg gtgtcgacaa gttggg 26

<210> 76
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gatctggtgg caattggag gaatgttcg 30

<210> 77
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<400> 77
cacgtactcg ccatacttt cgctcgag 28

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<400> 78

ccataactttt cgctcgcgga cgagctgtcc gtg

33

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<400> 79
gtataagaag cttattacgg cgatccaggc c

31

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<400> 80
cttcaagggc aagtacgcct ttttgaagac g

31

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29

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ctaattggatg tgtccgtttg atacggtag

29

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gtggaagaag tacgactacc ttcagtc 27

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gcccggttga cgcatcgcc agtgcagg 28

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cacacgacaa caccatggtt tccatcttc 29

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<400> 86
tggtgcctt tcgcccgcgcg agcctacttc 30

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tatatcatga gcgtgttcgt cgtgctactg ttc 33

<210> 88
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<400> 88
acccgactta caaagcgaat tctatagata tat 33

<210> 89
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<400> 89
acccttctta caaagcgaat tctatagata tat 33

<210> 90
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Met Gly Val Phe Val Val Leu Leu Ser Ile Ala Thr Leu Phe Gly Ser
-20 -15 -10

aca tcc ggt acc gcc ttg ggt cct cgt ggt aat tct cac tct tgt gac 96
Thr Ser Gly Thr Ala Leu Gly Pro Arg Gly Asn Ser His Ser Cys Asp
-5 -1 1 5

act gtt gac ggt ggt tac caa tgt ttc cca gaa att tct cac ttg tgg 144
Thr Val Asp Gly Gly Tyr Gln Cys Phe Pro Glu Ile Ser His Leu Trp
10 15 20 25

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ggt acc tac tct cca tac ttc tct ttg gca gac gaa tct gct att tct			192
Gly Thr Tyr Ser Pro Tyr Phe Ser Leu Ala Asp Glu Ser Ala Ile Ser			
30	35	40	
cca gac gtc cca aag gac tgt aga gtt act ttc gtt caa gtt ttg tct			240
Pro Asp Val Pro Lys Asp Cys Arg Val Thr Phe Val Gln Val Leu Ser			
45	50	55	
aga cac ggt gct aga tac cca act tct tct aag tct aag gct tac tct			288
Arg His Gly Ala Arg Tyr Pro Thr Ser Ser Lys Ser Lys Ala Tyr Ser			
60	65	70	
gct ttg att gaa gct att caa aag aac gct act gct ttc aag ggt aag			336
Ala Leu Ile Glu Ala Ile Gln Lys Asn Ala Thr Ala Phe Lys Gly Lys			
75	80	85	
tac gct ttc ttg aag act tac aac tac act ttg ggt gct gac gac ttg			384
Tyr Ala Phe Leu Lys Thr Tyr Asn Tyr Thr Leu Gly Ala Asp Asp Leu			
90	95	100	105
act cca ttc ggt gaa aac caa atg gtt aac tct ggt att aag ttc tac			432
Thr Pro Phe Gly Glu Asn Gln Met Val Asn Ser Gly Ile Lys Phe Tyr			
110	115	120	
aga aga tac aag gct ttg gct aga aag att gtt cca ttc att aga gct			480
Arg Arg Tyr Lys Ala Leu Ala Arg Lys Ile Val Pro Phe Ile Arg Ala			
125	130	135	
tct ggt tct gac aga gtt att gct tct gct gaa aag ttc att gaa ggt			528
Ser Gly Ser Asp Arg Val Ile Ala Ser Ala Glu Lys Phe Ile Glu Gly			
140	145	150	
ttc caa tct gct aag ttg gct gac cca ggt tct caa cca cac caa gct			576
Phe Gln Ser Ala Lys Leu Ala Asp Pro Gly Ser Gln Pro His Gln Ala			
155	160	165	
tct cca gtt att aac gtg atc att cca gaa gga tcc ggt tac aac aac			624
Ser Pro Val Ile Asn Val Ile Ile Pro Glu Gly Ser Gly Tyr Asn Asn			
170	175	180	185
act ttg gac cat ggt ctt tgt act gct ttc gaa gac tct acc cta ggt			672
Thr Leu Asp His Gly Leu Cys Thr Ala Phe Glu Asp Ser Thr Leu Gly			
190	195	200	
gac gac gtt gaa gct aac ttc act gct ttg ttc gct cca gct att aga			720
Asp Asp Val Glu Ala Asn Phe Thr Ala Leu Phe Ala Pro Ala Ile Arg			
205	210	215	
gct aga ttg gaa gct gac ttg cca ggt gtt act ttg act gac gaa gac			768
Ala Arg Leu Glu Ala Asp Leu Pro Gly Val Thr Leu Thr Asp Glu Asp			
220	225	230	
gtt gtt tac ttg atg gac atg tgt cca ttc gac act gtc gct aga act			816
Val Val Tyr Leu Met Asp Met Cys Pro Phe Asp Thr Val Ala Arg Thr			
235	240	245	
tct gac gct act gaa ttg tct cca ttc tgt gct ttg ttc act cac qac			864

Ser	Asp	Ala	Thr	Glu	Leu	Ser	Pro	Phe	Cys	Ala	Leu	Phe	Thr	His	Asp	
250				255					260				265			
gaa tgg atc caa tac gac tac ttg caa agc ttg ggt aag tac tac ggt															912	
Glu Trp Ile Gln Tyr Asp Tyr Leu Gln Ser Leu Gly Lys Tyr Tyr Gly																
270 275 280																
tac ggt gct ggt aac cca ttg ggt cca gct caa ggt gtt ggt ttc gct															960	
Tyr Gly Ala Gly Asn Pro Leu Gly Pro Ala Gln Gly Val Gly Phe Ala																
285 290 295																
aac gaa ttg att gct aga ttg act cac tct cca gtt caa gac cac act															1008	
Asn Glu Leu Ile Ala Arg Leu Thr His Ser Pro Val Gln Asp His Thr																
300 305 310																
tct act aac cac act ttg gac tct aac cca gct act ttc cca ttg aac															1056	
Ser Thr Asn His Thr Leu Asp Ser Asn Pro Ala Thr Phe Pro Leu Asn																
315 320 325																
gct act ttg tac gct gac ttc tct cac gac aac act atg ata tct att															1104	
Ala Thr Leu Tyr Ala Asp Phe Ser His Asp Asn Thr Met Ile Ser Ile																
330 335 340 345																
ttc ttc gct ttg ggt ttg tac aac ggt acc aag cca ttg tct act act															1152	
Phe Phe Ala Leu Gly Leu Tyr Asn Gly Thr Lys Pro Leu Ser Thr Thr																
350 355 360																
tct gtt gaa tct att gaa gaa act gac ggt tac tct gct tct tgg act															1200	
Ser Val Glu Ser Ile Glu Glu Thr Asp Gly Tyr Ser Ala Ser Trp Thr																
365 370 375																
gtt cca ttc gct gct aga gct tac gtt gaa atg atg caa tgt caa gct															1248	
Val Pro Phe Ala Ala Arg Ala Tyr Val Glu Met Met Gln Cys Gln Ala																
380 385 390																
gaa aag gaa cca ttg gtt aga gtt ttg gtt aac gac aga gtt gtt cca															1296	
Glu Lys Glu Pro Leu Val Arg Val Leu Val Asn Asp Arg Val Val Pro																
395 400 405																
ttg cac ggt tgt gct gtt gac aag ttg ggt aga tgt aag aga gac gac															1344	
Leu His Gly Cys Ala Val Asp Lys Leu Gly Arg Cys Lys Arg Asp Asp																
410 415 420 425																
ttc gtt gaa ggt ttg tct ttc gct aga tct ggt aac tgg gct gaa															1392	
Phe Val Glu Gly Leu Ser Phe Ala Arg Ser Gly Gly Asn Trp Ala Glu																
430 435 440																
tgt ttc gct taa															1404	
Cys Phe Ala																

<210> 91
<211> 467
<212> PRT
<213> Artificial Sequence

<220>

<223> Primer

<400> 91

Met Gly Val Phe Val Val Leu Leu Ser Ile Ala Thr Leu Phe Gly Ser
-20 -15 -10

Thr Ser Gly Thr Ala Leu Gly Pro Arg Gly Asn Ser His Ser Cys Asp
-5 -1 1 5

Thr Val Asp Gly Gly Tyr Gln Cys Phe Pro Glu Ile Ser His Leu Trp
10 15 20 25

Gly Thr Tyr Ser Pro Tyr Phe Ser Leu Ala Asp Glu Ser Ala Ile Ser
30 35 40

Pro Asp Val Pro Lys Asp Cys Arg Val Thr Phe Val Gln Val Leu Ser
45 50 55

Arg His Gly Ala Arg Tyr Pro Thr Ser Ser Lys Ser Lys Ala Tyr Ser
60 65 70

Ala Leu Ile Glu Ala Ile Gln Lys Asn Ala Thr Ala Phe Lys Gly Lys
75 80 85

Tyr Ala Phe Leu Lys Thr Tyr Asn Tyr Thr Leu Gly Ala Asp Asp Leu
90 95 100 105

Thr Pro Phe Gly Glu Asn Gln Met Val Asn Ser Gly Ile Lys Phe Tyr
110 115 120

Arg Arg Tyr Lys Ala Leu Ala Arg Lys Ile Val Pro Phe Ile Arg Ala
125 130 135

Ser Gly Ser Asp Arg Val Ile Ala Ser Ala Glu Lys Phe Ile Glu Gly
140 145 150

Phe Gln Ser Ala Lys Leu Ala Asp Pro Gly Ser Gln Pro His Gln Ala
155 160 165

Ser Pro Val Ile Asn Val Ile Ile Pro Glu Gly Ser Gly Tyr Asn Asn
170 175 180 185

Thr Leu Asp His Gly Leu Cys Thr Ala Phe Glu Asp Ser Thr Leu Gly
190 195 200

Asp Asp Val Glu Ala Asn Phe Thr Ala Leu Phe Ala Pro Ala Ile Arg
205 210 215

Ala Arg Leu Glu Ala Asp Leu Pro Gly Val Thr Leu Thr Asp Glu Asp
220 225 230

Val Val Tyr Leu Met Asp Met Cys Pro Phe Asp Thr Val Ala Arg Thr
235 240 245

Ser Asp Ala Thr Glu Leu Ser Pro Phe Cys Ala Leu Phe Thr His Asp
250 255 260 265

Glu Trp Ile Gln Tyr Asp Tyr Leu Gln Ser Leu Gly Lys Tyr Tyr Gly
270 275 280

Tyr Gly Ala Gly Asn Pro Leu Gly Pro Ala Gln Gly Val Gly Phe Ala
285 290 295

Asn Glu Leu Ile Ala Arg Leu Thr His Ser Pro Val Gln Asp His Thr
300 305 310

Ser Thr Asn His Thr Leu Asp Ser Asn Pro Ala Thr Phe Pro Leu Asn
315 320 325

Ala Thr Leu Tyr Ala Asp Phe Ser His Asp Asn Thr Met Ile Ser Ile
330 335 340 345

Phe Phe Ala Leu Gly Leu Tyr Asn Gly Thr Lys Pro Leu Ser Thr Thr
350 355 360

Ser Val Glu Ser Ile Glu Glu Thr Asp Gly Tyr Ser Ala Ser Trp Thr
365 370 375

Val Pro Phe Ala Ala Arg Ala Tyr Val Glu Met Met Gln Cys Gln Ala
380 385 390

Glu Lys Glu Pro Leu Val Arg Val Leu Val Asn Asp Arg Val Val Pro
395 400 405

Leu His Gly Cys Ala Val Asp Lys Leu Gly Arg Cys Lys Arg Asp Asp

410

415

420

425

Phe Val Glu Gly Leu Ser Phe Ala Arg Ser Gly Gly Asn Trp Ala Glu
430 435 440

Cys Phe Ala

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<210> 92
<211> 1404
<212> DNA
<213> Artificial Sequence
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<220>
<223> Synthetic

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<220>
<221> sig_peptide
<222> (1)..(69)
<223>
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<220>
<221> CDS
<222> (1)..(1401)
<223>

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<220>
<221> mat_peptide
<222> (70)..()
<223>
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<400> 92
atg ggc gtg ttc gtc gtg cta ctg tcc att gcc acc ttg ttc ggt tcc
Met Gly Val Phe Val Val Leu Leu Ser Ile Ala Thr Leu Phe Gly Ser
-20          -15          -10

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aca tcc ggt acc gcc ttg ggt cct cgt ggt aat tct cac tct tgt gac 96
Thr Ser Gly Thr Ala Leu Gly Pro Arg Gly Asn Ser His Ser Cys Asp
-5          -1   1           5

```

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act gtt gac ggt ggt tac caa tgt ttc cca gaa att tct cac ttg tgg      144
Thr Val Asp Gly Gly Tyr Gln Cys Phe Pro Glu Ile Ser His Leu Trp
10          15           20           25

```

ggt acc tac tct cca tac ttc tct ttg gca gac gaa tct gct att tct
 Gly Thr Tyr Ser Pro Tyr Phe Ser Leu Ala Asp Glu Ser Ala Ile Ser
 30 35 40

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cca gac gtc cca aag gac tgt aga gtt act ttc gtt caa gtt ttg tct      240
Pro Asp Val Pro Lys Asp Cys Arg Val Thr Phe Val Gln Val Leu Ser
        45          50          55

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aga cac ggt gct aga tac cca act tct tct gcg tct aag gct tac tct 288
Arg His Gly Ala Arg Tyr Pro Thr Ser Ser Ala Ser Lys Ala Tyr Ser

60	65	70	
gct ttg att gaa gct att caa aag aac gct act gct ttc aag ggt aag Ala Leu Ile Glu Ala Ile Gln Lys Asn Ala Thr Ala Phe Lys Gly Lys 75	80	85	336
tac gct ttc ttg aag act tac aac tac act ttg ggt gct gac gac ttg Tyr Ala Phe Leu Lys Thr Tyr Asn Tyr Thr Leu Gly Ala Asp Asp Leu 90	95	100	384
act cca ttc ggt gaa aac caa atg gtt aac tct ggt att aag ttc tac Thr Pro Phe Gly Glu Asn Gln Met Val Asn Ser Gly Ile Lys Phe Tyr 110	115	120	432
aga aga tac aag gct ttg gct aga aag att gtt cca ttc att aga gct Arg Arg Tyr Lys Ala Leu Ala Arg Lys Ile Val Pro Phe Ile Arg Ala 125	130	135	480
tct ggt tct gac aga gtt att gct tct gct gaa aag ttc att gaa ggt Ser Gly Ser Asp Arg Val Ile Ala Ser Ala Glu Lys Phe Ile Glu Gly 140	145	150	528
ttc caa tct gct aag ttg gct gac cca ggt tct caa cca cac caa gct Phe Gln Ser Ala Lys Leu Ala Asp Pro Gly Ser Gln Pro His Gln Ala 155	160	165	576
tct cca gtt att aac gtg atc att cca gaa gga tcc ggt tac aac aac Ser Pro Val Ile Asn Val Ile Ile Pro Glu Gly Ser Gly Tyr Asn Asn 170	175	180	624
act ttg gac cat ggt ctt tgt act gct ttc gaa gac tct acc cta ggt Thr Leu Asp His Gly Leu Cys Thr Ala Phe Glu Asp Ser Thr Leu Gly 190	195	200	672
gac gac gtt gaa gct aac ttc act gct ttg ttc gct cca gct att aga Asp Asp Val Glu Ala Asn Phe Thr Ala Leu Phe Ala Pro Ala Ile Arg 205	210	215	720
gct aga ttg gaa gct gac ttg cca ggt gtt act ttg act gac gaa gac Ala Arg Leu Glu Ala Asp Leu Pro Gly Val Thr Leu Thr Asp Glu Asp 220	225	230	768
gtt gtt tac ttg atg gac atg tgt cca ttc gac act gtc gct aga act Val Val Tyr Leu Met Asp Met Cys Pro Phe Asp Thr Val Ala Arg Thr 235	240	245	816
tct gac gct act gaa ttg tct cca ttc tgt gct ttg ttc act cac gac Ser Asp Ala Thr Glu Leu Ser Pro Phe Cys Ala Leu Phe Thr His Asp 250	255	260	864
gaa tgg atc caa tac gac tac ttg caa agc ttg ggt aag tac tac ggt Glu Trp Ile Gln Tyr Asp Tyr Leu Gln Ser Leu Gly Lys Tyr Tyr Gly 270	275	280	912
tac ggt gct ggt aac cca ttg ggt cca gct caa ggt gtt ggt ttc gct Tyr Gly Ala Gly Asn Pro Leu Gly Pro Ala Gln Gly Val Gly Phe Ala 285	290	295	960

aac gaa ttg att gct aga ttg act cac tct cca gtt caa gac cac act Asn Glu Leu Ile Ala Arg Leu Thr His Ser Pro Val Gln Asp His Thr 300 305 310	1008
tct act aac cac act ttg gac tct aac cca gct act ttc cca ttg aac Ser Thr Asn His Thr Leu Asp Ser Asn Pro Ala Thr Phe Pro Leu Asn 315 320 325	1056
gct act ttg tac gct gac ttc tct cac gac aac act atg ata tct att Ala Thr Leu Tyr Ala Asp Phe Ser His Asp Asn Thr Met Ile Ser Ile 330 335 340 345	1104
ttc ttc gct ttg ggt ttg tac aac ggt acc aag cca ttg tct act act Phe Phe Ala Leu Gly Leu Tyr Asn Gly Thr Lys Pro Leu Ser Thr Thr 350 355 360	1152
tct gtt gaa tct att gaa gaa act gac ggt tac tct gct tct tgg act Ser Val Glu Ser Ile Glu Glu Thr Asp Gly Tyr Ser Ala Ser Trp Thr 365 370 375	1200
gtt cca ttc gct gct aga gct tac gtt gaa atg atg caa tgt caa gct Val Pro Phe Ala Ala Arg Ala Tyr Val Glu Met Met Gln Cys Gln Ala 380 385 390	1248
gaa aag gaa cca ttg gtt aga gtt ttg gtt aac gac aga gtt gtt cca Glu Lys Glu Pro Leu Val Arg Val Leu Val Asn Asp Arg Val Val Pro 395 400 405	1296
ttg cac ggt tgt gct gtt gac aag ttg ggt aga tgt aag aga gac gac Leu His Gly Cys Ala Val Asp Lys Leu Gly Arg Cys Lys Arg Asp Asp 410 415 420 425	1344
ttc gtt gaa ggt ttg tct ttc gct aga tct ggt aac tgg gct gaa Phe Val Glu Gly Leu Ser Phe Ala Arg Ser Gly Gly Asn Trp Ala Glu 430 435 440	1392
tgt ttc gct taa Cys Phe Ala	1404

<210> 93
<211> 467
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 93

Met Gly Val Phe Val Val Leu Leu Ser Ile Ala Thr Leu Phe Gly Ser
-20 -15 -10

Thr Ser Gly Thr Ala Leu Gly Pro Arg Gly Asn Ser His Ser Cys Asp

-5

-1 1

5

Thr Val Asp Gly Gly Tyr Gln Cys Phe Pro Glu Ile Ser His Leu Trp
10 15 20 25

Gly Thr Tyr Ser Pro Tyr Phe Ser Leu Ala Asp Glu Ser Ala Ile Ser
30 35 40

Pro Asp Val Pro Lys Asp Cys Arg Val Thr Phe Val Gln Val Leu Ser
45 50 55

Arg His Gly Ala Arg Tyr Pro Thr Ser Ser Ala Ser Lys Ala Tyr Ser
60 65 70

Ala Leu Ile Glu Ala Ile Gln Lys Asn Ala Thr Ala Phe Lys Gly Lys
75 85

Tyr Ala Phe Leu Lys Thr Tyr Asn Tyr Thr Leu Gly Ala Asp Asp Leu
90 95 100 105

Thr Pro Phe Gly Glu Asn Gln Met Val Asn Ser Gly Ile Lys Phe Tyr
110 115 120

Arg Arg Tyr Lys Ala Leu Ala Arg Lys Ile Val Pro Phe Ile Arg Ala
125 130 135

Ser Gly Ser Asp Arg Val Ile Ala Ser Ala Glu Lys Phe Ile Glu Gly
140 145 150

Phe Gln Ser Ala Lys Leu Ala Asp Pro Gly Ser Gln Pro His Gln Ala
155 160 165

Ser Pro Val Ile Asn Val Ile Ile Pro Glu Gly Ser Gly Tyr Asn Asn
170 175 180 185

Thr Leu Asp His Gly Leu Cys Thr Ala Phe Glu Asp Ser Thr Leu Gly
190 195 200

Asp Asp Val Glu Ala Asn Phe Thr Ala Leu Phe Ala Pro Ala Ile Arg
205 210 215

Ala Arg Leu Glu Ala Asp Leu Pro Gly Val Thr Leu Thr Asp Glu Asp
220 225 230

Val Val Tyr Leu Met Asp Met Cys Pro Phe Asp Thr Val Ala Arg Thr
235 240 245

Ser Asp Ala Thr Glu Leu Ser Pro Phe Cys Ala Leu Phe Thr His Asp
250 255 260 265

Glu Trp Ile Gln Tyr Asp Tyr Leu Gln Ser Leu Gly Lys Tyr Tyr Gly
270 275 280

Tyr Gly Ala Gly Asn Pro Leu Gly Pro Ala Gln Gly Val Gly Phe Ala
285 290 295

Asn Glu Leu Ile Ala Arg Leu Thr His Ser Pro Val Gln Asp His Thr
300 305 310

Ser Thr Asn His Thr Leu Asp Ser Asn Pro Ala Thr Phe Pro Leu Asn
315 320 325

Ala Thr Leu Tyr Ala Asp Phe Ser His Asp Asn Thr Met Ile Ser Ile
330 335 340 345

Phe Phe Ala Leu Gly Leu Tyr Asn Gly Thr Lys Pro Leu Ser Thr Thr
350 355 360

Ser Val Glu Ser Ile Glu Glu Thr Asp Gly Tyr Ser Ala Ser Trp Thr
365 370 375

Val Pro Phe Ala Ala Arg Ala Tyr Val Glu Met Met Gln Cys Gln Ala
380 385 390

Glu Lys Glu Pro Leu Val Arg Val Leu Val Asn Asp Arg Val Val Pro
395 400 405

Leu His Gly Cys Ala Val Asp Lys Leu Gly Arg Cys Lys Arg Asp Asp
410 415 420 425

Phe Val Glu Gly Leu Ser Phe Ala Arg Ser Gly Gly Asn Trp Ala Glu
430 435 440

Cys Phe Ala

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<210> 94
<211> 1404
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<220>
<221> sig_peptide
<222> (1)..(69)
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<220>
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<223>

<220>
<221> mat_peptide
<222> (70)..()
<223>

<400> 94
atg ggc gtg ttc gtc gtg cta ctg tcc att gcc acc ttg ttc ggt tcc      48
Met Gly Val Phe Val Val Leu Leu Ser Ile Ala Thr Leu Phe Gly Ser
-20          -15          -10

aca tcc ggt acc gcc ttg ggt cct cgt ggt aat tct cac tct tgt gac      96
Thr Ser Gly Thr Ala Leu Gly Pro Arg Gly Asn Ser His Ser Cys Asp
-5           -1   1           5

act gtt gac ggt ggt tac caa tgt ttc cca gaa att tct cac ttg tgg      144
Thr Val Asp Gly Gly Tyr Gln Cys Phe Pro Glu Ile Ser His Leu Trp
10          15          20          25

ggt aca tac tct cca ttc ttc tct ttg gct gac gaa tct gct att tct      192
Gly Thr Tyr Ser Pro Phe Phe Ser Leu Ala Asp Glu Ser Ala Ile Ser
30          35          40

cca gac gtt cca aag ggt tgt aga gtt act ttc gtt caa gtt ttg tct      240
Pro Asp Val Pro Lys Gly Cys Arg Val Thr Phe Val Gln Val Leu Ser
45          50          55

aga cac ggt gct aga tac cca act tct tct aag tct aag gct tac tct      288
Arg His Gly Ala Arg Tyr Pro Thr Ser Ser Lys Ser Lys Ala Tyr Ser
60          65          70

gct ttg att gaa gct att caa aag aac gct act gct ttc aag ggt aag      336
Ala Leu Ile Glu Ala Ile Gln Lys Asn Ala Thr Ala Phe Lys Gly Lys
75          80          85

tac gct ttc ttg aag act tac aat tac act ttg ggt gct gac gac ttg      384
Tyr Ala Phe Leu Lys Thr Tyr Asn Tyr Thr Leu Gly Ala Asp Asp Leu
90          95          100         105

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act cca ttc ggt gaa caa caa atg aac tct ggt att aag ttc tac Thr Pro Phe Gly Glu Gln Gln Met Val Asn Ser Gly Ile Lys Phe Tyr 110 115 120	432
aga aga tac aag gct ttg gct aga aag att gtt cca ttc att aga gct Arg Arg Tyr Lys Ala Leu Ala Arg Lys Ile Val Pro Phe Ile Arg Ala 125 130 135	480
tct ggt tct gac aga gtt att gct tct gcc gaa aag ttc att gaa ggt Ser Gly Ser Asp Arg Val Ile Ala Ser Ala Glu Lys Phe Ile Glu Gly 140 145 150	528
ttc caa tct gct aag ttg gct gac cca ggt gct aac cca cac caa gct Phe Gln Ser Ala Lys Leu Ala Asp Pro Gly Ala Asn Pro His Gln Ala 155 160 165	576
tct cca gtt att aac gtt att att cca gaa ggt gct ggt tac aac aac Ser Pro Val Ile Asn Val Ile Ile Pro Glu Gly Ala Gly Tyr Asn Asn 170 175 180 185	624
act ttg gac cac ggt ttg tgt act gct ttc gaa gaa tct acc cta ggt Thr Leu Asp His Gly Leu Cys Thr Ala Phe Glu Glu Ser Thr Leu Gly 190 195 200	672
gac gac gtt gaa gct aac ttc act gct gtt ttc gct cca cca att aga Asp Asp Val Glu Ala Asn Phe Thr Ala Val Phe Ala Pro Pro Ile Arg 205 210 215	720
gct aga ttg gaa gct cac ttg cca ggt gtt aac ttg act gac gaa gac Ala Arg Leu Glu Ala His Leu Pro Gly Val Asn Leu Thr Asp Glu Asp 220 225 230	768
gtt gtt aac ttg atg gac atg tgt cca ttc gac act gtt gct aga act Val Val Asn Leu Met Asp Met Cys Pro Phe Asp Thr Val Ala Arg Thr 235 240 245	816
tct gac gct act caa ttg tct cca ttc tgt gac ttg ttc act cac gac Ser Asp Ala Thr Gln Leu Ser Pro Phe Cys Asp Leu Phe Thr His Asp 250 255 260 265	864
gaa tgg att caa tac gac tac ttg caa tct ttg ggt aag tac tac ggt Glu Trp Ile Gln Tyr Asp Tyr Leu Gln Ser Leu Gly Lys Tyr Tyr Gly 270 275 280	912
tac ggt gct ggt aac cca ttg ggt cca gct caa ggt gtt ggt ttc gtt Tyr Gly Ala Gly Asn Pro Leu Gly Pro Ala Gln Gly Val Gly Phe Val 285 290 295	960
aac gaa ttg att gct aga ttg act cac tct cca gtt caa gac cac act Asn Glu Leu Ile Ala Arg Leu Thr His Ser Pro Val Gln Asp His Thr 300 305 310	1008
tct act aac cac act ttg gac tct aac cca gct act ttc cca ttg aac Ser Thr Asn His Thr Leu Asp Ser Asn Pro Ala Thr Phe Pro Leu Asn 315 320 325	1056
gct act ttg tac gct gac ttc tct cac gac aac act atg gtt tct att	1104

Ala Thr Leu Tyr Ala Asp Phe Ser His Asp Asn Thr Met Val Ser Ile			
330	335	340	345
ttc ttc gct ttg ggt ttg tac aac ggt act aag cca ttg tct act act			1152
Phe Phe Ala Leu Gly Leu Tyr Asn Gly Thr Lys Pro Leu Ser Thr Thr			
350	355	360	
tct gtt gaa tct att gaa gaa act gac ggt tac tct gct tct tgg act			1200
Ser Val Glu Ser Ile Glu Glu Thr Asp Gly Tyr Ser Ala Ser Trp Thr			
365	370	375	
gtt cca ttc gct gct aga gct tac gtt gaa atg atg caa tgt gaa gct			1248
Val Pro Phe Ala Ala Arg Ala Tyr Val Glu Met Met Gln Cys Glu Ala			
380	385	390	
gaa aag gaa cca ttg gtt aga gtt ttg gtt aac gac aga gtt gtt cca			1296
Glu Lys Glu Pro Leu Val Arg Val Leu Val Asn Asp Arg Val Val Pro			
395	400	405	
ttg cac ggt tgt gct gtt gac aag ttg ggt aga tgt aag aga gac gac			1344
Leu His Gly Cys Ala Val Asp Lys Leu Gly Arg Cys Lys Arg Asp Asp			
410	415	420	425
ttc gtt gaa ggt ttg tct ttc gct aga tct ggt aac tgg gaa gaa			1392
Phe Val Glu Gly Leu Ser Phe Ala Arg Ser Gly Gly Asn Trp Glu Glu			
430	435	440	
tgt ttc gct taa			1404
Cys Phe Ala			

<210> 95
<211> 467
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 95

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-20 -15 -10

Thr Ser Gly Thr Ala Leu Gly Pro Arg Gly Asn Ser His Ser Cys Asp
-5 -1 1 5

Thr Val Asp Gly Gly Tyr Gln Cys Phe Pro Glu Ile Ser His Leu Trp
10 15 20 25

Gly Thr Tyr Ser Pro Phe Phe Ser Leu Ala Asp Glu Ser Ala Ile Ser
30 35 40

Pro Asp Val Pro Lys Gly Cys Arg Val Thr Phe Val Gln Val Leu Ser
45 50 55

Arg His Gly Ala Arg Tyr Pro Thr Ser Ser Lys Ser Lys Ala Tyr Ser
60 65 70

Ala Leu Ile Glu Ala Ile Gln Lys Asn Ala Thr Ala Phe Lys Gly Lys
75 80 85

Tyr Ala Phe Leu Lys Thr Tyr Asn Tyr Thr Leu Gly Ala Asp Asp Leu
90 95 100 105

Thr Pro Phe Gly Glu Gln Gln Met Val Asn Ser Gly Ile Lys Phe Tyr
110 115 120

Arg Arg Tyr Lys Ala Leu Ala Arg Lys Ile Val Pro Phe Ile Arg Ala
125 130 135

Ser Gly Ser Asp Arg Val Ile Ala Ser Ala Glu Lys Phe Ile Glu Gly
140 145 150

Phe Gln Ser Ala Lys Leu Ala Asp Pro Gly Ala Asn Pro His Gln Ala
155 160 165

Ser Pro Val Ile Asn Val Ile Ile Pro Glu Gly Ala Gly Tyr Asn Asn
170 175 180 185

Thr Leu Asp His Gly Leu Cys Thr Ala Phe Glu Glu Ser Thr Leu Gly
190 195 200

Asp Asp Val Glu Ala Asn Phe Thr Ala Val Phe Ala Pro Pro Ile Arg
205 210 215

Ala Arg Leu Glu Ala His Leu Pro Gly Val Asn Leu Thr Asp Glu Asp
220 225 230

Val Val Asn Leu Met Asp Met Cys Pro Phe Asp Thr Val Ala Arg Thr
235 240 245

Ser Asp Ala Thr Gln Leu Ser Pro Phe Cys Asp Leu Phe Thr His Asp
250 255 260 265

Glu Trp Ile Gln Tyr Asp Tyr Leu Gln Ser Leu Gly Lys Tyr Tyr Gly
270 275 280

Tyr Gly Ala Gly Asn Pro Leu Gly Pro Ala Gln Gly Val Gly Phe Val
285 290 295

Asn Glu Leu Ile Ala Arg Leu Thr His Ser Pro Val Gln Asp His Thr
300 305 310

Ser Thr Asn His Thr Leu Asp Ser Asn Pro Ala Thr Phe Pro Leu Asn
315 320 325

Ala Thr Leu Tyr Ala Asp Phe Ser His Asp Asn Thr Met Val Ser Ile
330 335 340 345

Phe Phe Ala Leu Gly Leu Tyr Asn Gly Thr Lys Pro Leu Ser Thr Thr
350 355 360

Ser Val Glu Ser Ile Glu Glu Thr Asp Gly Tyr Ser Ala Ser Trp Thr
365 370 375

Val Pro Phe Ala Ala Arg Ala Tyr Val Glu Met Met Gln Cys Glu Ala
380 385 390

Glu Lys Glu Pro Leu Val Arg Val Leu Val Asn Asp Arg Val Val Pro
395 400 405

Leu His Gly Cys Ala Val Asp Lys Leu Gly Arg Cys Lys Arg Asp Asp
410 415 420 425

Phe Val Glu Gly Leu Ser Phe Ala Arg Ser Gly Gly Asn Trp Glu Glu
430 435 440

Cys Phe Ala

<210> 96
<211> 1404
<212> DNA
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<220>
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<220>

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<221> sig_peptide
<222> (1)..(69)
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<221> CDS
<222> (1)..(1401)
<223>

<220>
<221> mat_peptide
<222> (70)..()
<223>

<400> 96
atg ggc gtg ttc gtc gtg cta ctg tcc att gcc acc ttg ttc ggt tcc      48
Met Gly Val Phe Val Val Leu Leu Ser Ile Ala Thr Leu Phe Gly Ser
-20          -15          -10

aca tcc ggt acc gcc ttg ggt cct cgt ggt aat tct cac tct tgt gac      96
Thr Ser Gly Thr Ala Leu Gly Pro Arg Gly Asn Ser His Ser Cys Asp
-5           -1   1           5

act gtt gac ggt ggt tac caa tgg ttc cca gaa att tct cac ttg tgg      144
Thr Val Asp Gly Gly Tyr Gln Cys Phe Pro Glu Ile Ser His Leu Trp
10          15          20          25

ggt aca tac tct cca ttc ttc tct ttg gct gac gaa tct gct att tct      192
Gly Thr Tyr Ser Pro Phe Phe Ser Leu Ala Asp Glu Ser Ala Ile Ser
30          35          40

cca gac gtt cca aag ggt tgg aga gtt act ttc gtt caa gtt ttg tct      240
Pro Asp Val Pro Lys Gly Cys Arg Val Thr Phe Val Gln Val Leu Ser
45          50          55

aga cac ggt gct aga tac cca act tct tct gcg tct aag gct tac tct      288
Arg His Gly Ala Arg Tyr Pro Thr Ser Ser Ala Ser Lys Ala Tyr Ser
60          65          70

gct ttg att gaa gct att caa aag aac gct act gct ttc aag ggt aag      336
Ala Leu Ile Glu Ala Ile Gln Lys Asn Ala Thr Ala Phe Lys Gly Lys
75          80          85

tac gct ttc ttg aag act tac aat tac act ttg ggt gct gac gac ttg      384
Tyr Ala Phe Leu Lys Thr Tyr Asn Tyr Thr Leu Gly Ala Asp Asp Leu
90          95          100         105

act cca ttc ggt gaa caa caa atg gtt aac tct ggt att aag ttc tac      432
Thr Pro Phe Gly Glu Gln Gln Met Val Asn Ser Gly Ile Lys Phe Tyr
110         115         120

aga aga tac aag gct ttg gct aga aag att gtt cca ttc att aga gct      480
Arg Arg Tyr Lys Ala Leu Ala Arg Lys Ile Val Pro Phe Ile Arg Ala
125         130         135

tct ggt tct gac aga gtt att gct tct gcc gaa aag ttc att gaa ggt      528
Ser Gly Ser Asp Arg Val Ile Ala Ser Ala Glu Lys Phe Ile Glu Gly

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140	145	150	
ttc caa tct gct aag ttg gct gac cca ggt gct aac cca cac caa gct Phe Gln Ser Ala Lys Leu Ala Asp Pro Gly Ala Asn Pro His Gln Ala			576
155	160	165	
tct cca gtt att aac gtt att att cca gaa ggt gct ggt tac aac aac Ser Pro Val Ile Asn Val Ile Ile Pro Glu Gly Ala Gly Tyr Asn Asn			624
170	175	180	185
act ttg gac cac ggt ttg tgt act gct ttc gaa gaa tct acc cta ggt Thr Leu Asp His Gly Leu Cys Thr Ala Phe Glu Glu Ser Thr Leu Gly			672
190	195	200	
gac gac gtt gaa gct aac ttc act gct gtt ttc gct cca cca att aga Asp Asp Val Glu Ala Asn Phe Thr Ala Val Phe Ala Pro Pro Ile Arg			720
205	210	215	
gct aga ttg gaa gct cac ttg cca ggt gtt aac ttg act gac gaa gac Ala Arg Leu Glu Ala His Leu Pro Gly Val Asn Leu Thr Asp Glu Asp			768
220	225	230	
gtt gtt aac ttg atg gac atg tgt cca ttc gac act gtt gct aga act Val Val Asn Leu Met Asp Met Cys Pro Phe Asp Thr Val Ala Arg Thr			816
235	240	245	
tct gac gct act caa ttg tct cca ttc tgt gac ttg ttc act cac gac Ser Asp Ala Thr Gln Leu Ser Pro Phe Cys Asp Leu Phe Thr His Asp			864
250	255	260	265
gaa tgg att caa tac gac tac ttg caa tct ttg ggt aag tac tac ggt Glu Trp Ile Gln Tyr Asp Tyr Leu Gln Ser Leu Gly Lys Tyr Tyr Gly			912
270	275	280	
tac ggt gct ggt aac cca ttg ggt cca gct caa ggt gtt ggt ttc gtt Tyr Gly Ala Gly Asn Pro Leu Gly Pro Ala Gln Gly Val Gly Phe Val			960
285	290	295	
aac gaa ttg att gct aga ttg act cac tct cca gtt caa gac cac act Asn Glu Leu Ile Ala Arg Leu Thr His Ser Pro Val Gln Asp His Thr			1008
300	305	310	
tct act aac cac act ttg gac tct aac cca gct act ttc cca ttg aac Ser Thr Asn His Thr Leu Asp Ser Asn Pro Ala Thr Phe Pro Leu Asn			1056
315	320	325	
gct act ttg tac gct gac ttc tct cac gac aac act atg gtt tct att Ala Thr Leu Tyr Ala Asp Phe Ser His Asp Asn Thr Met Val Ser Ile			1104
330	335	340	345
ttc ttc gct ttg ggt ttg tac aac ggt act aag cca ttg tct act act Phe Phe Ala Leu Gly Leu Tyr Asn Gly Thr Lys Pro Leu Ser Thr Thr			1152
350	355	360	
tct gtt gaa tct att gaa gaa act gac ggt tac tct gct tct ttg act Ser Val Glu Ser Ile Glu Glu Thr Asp Gly Tyr Ser Ala Ser Trp Thr			1200
365	370	375	

gtt cca ttc gct gct aga gct tac gtt gaa atg atg caa tgt gaa gct		1248
Val Pro Phe Ala Ala Arg Ala Tyr Val Glu Met Met Gln Cys Glu Ala		
380	385	390
gaa aag gaa cca ttg gtt aga gtt ttg gtt aac gac aga gtt gtt cca		1296
Glu Lys Glu Pro Leu Val Arg Val Leu Val Asn Asp Arg Val Val Pro		
395	400	405
ttg cac ggt tgt gct gac aag ttg ggt aga tgt aag aga gac gac		1344
Leu His Gly Cys Ala Val Asp Lys Leu Gly Arg Cys Lys Arg Asp Asp		
410	415	420
425		
ttc gtt gaa ggt ttg tct ttc gct aga tct ggt aac tgg gaa gaa		1392
Phe Val Glu Gly Leu Ser Phe Ala Arg Ser Gly Gly Asn Trp Glu Glu		
430	435	440
tgt ttc gct taa		1404
Cys Phe Ala		

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<211> 467
<212> PRT
<213> Artificial Sequence

<220>
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<400> 97

Met Gly Val Phe Val Val Leu Leu Ser Ile Ala Thr Leu Phe Gly Ser
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Thr Ser Gly Thr Ala Leu Gly Pro Arg Gly Asn Ser His Ser Cys Asp
-5 -1 1 5

Thr Val Asp Gly Gly Tyr Gln Cys Phe Pro Glu Ile Ser His Leu Trp
10 15 20 25

Gly Thr Tyr Ser Pro Phe Phe Ser Leu Ala Asp Glu Ser Ala Ile Ser
 30 35 40

Pro Asp Val Pro Lys Gly Cys Arg Val Thr Phe Val Gln Val Leu Ser
 45 50 55

Arg His Gly Ala Arg Tyr Pro Thr Ser Ser Ala Ser Lys Ala Tyr Ser
 60 65 70

Ala Leu Ile Glu Ala Ile Gln Lys Asn Ala Thr Ala Phe Lys Gly Lys

75

80

85

Tyr Ala Phe Leu Lys Thr Tyr Asn Tyr Thr Leu Gly Ala Asp Asp Leu
90 95 100 105

Thr Pro Phe Gly Glu Gln Gln Met Val Asn Ser Gly Ile Lys Phe Tyr
110 115 120

Arg Arg Tyr Lys Ala Leu Ala Arg Lys Ile Val Pro Phe Ile Arg Ala
125 130 135

Ser Gly Ser Asp Arg Val Ile Ala Ser Ala Glu Lys Phe Ile Glu Gly
140 145 150

Phe Gln Ser Ala Lys Leu Ala Asp Pro Gly Ala Asn Pro His Gln Ala
155 160 165

Ser Pro Val Ile Asn Val Ile Ile Pro Glu Gly Ala Gly Tyr Asn Asn
170 175 180 185

Thr Leu Asp His Gly Leu Cys Thr Ala Phe Glu Glu Ser Thr Leu Gly
190 195 200

Asp Asp Val Glu Ala Asn Phe Thr Ala Val Phe Ala Pro Pro Ile Arg
205 210 215

Ala Arg Leu Glu Ala His Leu Pro Gly Val Asn Leu Thr Asp Glu Asp
220 225 230

Val Val Asn Leu Met Asp Met Cys Pro Phe Asp Thr Val Ala Arg Thr
235 240 245

Ser Asp Ala Thr Gln Leu Ser Pro Phe Cys Asp Leu Phe Thr His Asp
250 255 260 265

Glu Trp Ile Gln Tyr Asp Tyr Leu Gln Ser Leu Gly Lys Tyr Tyr Gly
270 275 280

Tyr Gly Ala Gly Asn Pro Leu Gly Pro Ala Gln Gly Val Gly Phe Val
285 290 295

Asn Glu Leu Ile Ala Arg Leu Thr His Ser Pro Val Gln Asp His Thr
300 305 310

Ser Thr Asn His Thr Leu Asp Ser Asn Pro Ala Thr Phe Pro Leu Asn
315 320 325

Ala Thr Leu Tyr Ala Asp Phe Ser His Asp Asn Thr Met Val Ser Ile
330 335 340 345

Phe Phe Ala Leu Gly Leu Tyr Asn Gly Thr Lys Pro Leu Ser Thr Thr
350 355 360

Ser Val Glu Ser Ile Glu Glu Thr Asp Gly Tyr Ser Ala Ser Trp Thr
365 370 375

Val Pro Phe Ala Ala Arg Ala Tyr Val Glu Met Met Gln Cys Glu Ala
380 385 390

Glu Lys Glu Pro Leu Val Arg Val Leu Val Asn Asp Arg Val Val Pro
395 400 405

Leu His Gly Cys Ala Val Asp Lys Leu Gly Arg Cys Lys Arg Asp Asp
410 415 420 425

Phe Val Glu Gly Leu Ser Phe Ala Arg Ser Gly Gly Asn Trp Glu Glu
430 435 440

Cys Phe Ala

<210> 98
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Glu Ile Ser His Leu Trp Gly Gln Tyr Ser Pro Tyr Phe Ser Leu Glu
20 25 30

Asp Glu Ser Ala Ile Ser Pro Asp Val Pro Asp Asp Cys Arg Val Thr

35

40

45

Phe Val Gln Val Leu Ser Arg His Gly Ala Arg Tyr Pro Thr Ser Ser
50 55 60

Lys Ser Lys Ala Tyr Ser Ala Leu Ile Glu Ala Ile Gln Lys Asn Ala
65 70 75 80

Thr Ala Phe Lys Gly Lys Tyr Ala Phe Leu Lys Thr Tyr Asn Tyr Thr
85 90 95

Leu Gly Ala Asp Asp Leu Thr Pro Phe Gly Glu Asn Gln Met Val Asn
100 105 110

Ser Gly Ile Lys Phe Tyr Arg Arg Tyr Lys Ala Leu Ala Arg Lys Ile
115 120 125

Val Pro Phe Ile Arg Ala Ser Gly Ser Asp Arg Val Ile Ala Ser Ala
130 135 140

Glu Lys Phe Ile Glu Gly Phe Gln Ser Ala Lys Leu Ala Asp Pro Gly
145 150 155 160

Ser Gln Pro His Gln Ala Ser Pro Val Ile Asp Val Ile Ile Pro Glu
165 170 175

Gly Ser Gly Tyr Asn Asn Thr Leu Asp His Gly Thr Cys Thr Ala Phe
180 185 190

Glu Asp Ser Glu Leu Gly Asp Asp Val Glu Ala Asn Phe Thr Ala Leu
195 200 205

Phe Ala Pro Ala Ile Arg Ala Arg Leu Glu Ala Asp Leu Pro Gly Val
210 215 220

Thr Leu Thr Asp Glu Asp Val Val Tyr Leu Met Asp Met Cys Pro Phe
225 230 235 240

Glu Thr Val Ala Arg Thr Ser Asp Ala Thr Glu Leu Ser Pro Phe Cys
245 250 255

Ala Leu Phe Thr His Asp Glu Trp Arg Gln Tyr Asp Tyr Leu Gln Ser
260 265 270

Leu Gly Lys Tyr Tyr Gly Tyr Gly Ala Gly Asn Pro Leu Gly Pro Ala
275 280 285

Gln Gly Val Gly Phe Ala Asn Glu Leu Ile Ala Arg Leu Thr Arg Ser
290 295 300

Pro Val Gln Asp His Thr Ser Thr Asn His Thr Leu Asp Ser Asn Pro
305 310 315 320

Ala Thr Phe Pro Leu Asn Ala Thr Leu Tyr Ala Asp Phe Ser His Asp
325 330 335

Asn Ser Met Ile Ser Ile Phe Phe Ala Leu Gly Leu Tyr Asn Gly Thr
340 345 350

Ala Pro Leu Ser Thr Thr Ser Val Glu Ser Ile Glu Glu Thr Asp Gly
355 360 365

Tyr Ser Ala Ser Trp Thr Val Pro Phe Gly Ala Arg Ala Tyr Val Glu
370 375 380

Met Met Gln Cys Gln Ala Glu Lys Glu Pro Leu Val Arg Val Leu Val
385 390 395 400

Asn Asp Arg Val Val Pro Leu His Gly Cys Ala Val Asp Lys Leu Gly
405 410 415

Arg Cys Lys Arg Asp Asp Phe Val Glu Gly Leu Ser Phe Ala Arg Ser
420 425 430

Gly Gly Asn Trp Ala Glu Cys Phe Ala
435 440